GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: July 3, 2006, 06:14:25 ; Search time 1956 Seconds
(without alignments)
555.780 Million cell updates/sec

Title: US-10-615-497-9
Perfect score: 17
Sequence: 1 cgcatctcccaccccca 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 69

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
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9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	100.0	41	2	CS138234	CS138234 Sequence
2	17	100.0	51	2	AX427056	AX427056 Sequence
3	17	100.0	51	2	AX427057	AX427057 Sequence
4	17	100.0	201	2	CQ815154	CQ815154 Sequence
5	17	100.0	201	2	CQ815155	CQ815155 Sequence
6	17	100.0	483	2	CQ787686	CQ787686 Sequence
7	17	100.0	483	2	CS138211	CS138211 Sequence
8	17	100.0	484	2	CQ787685	CQ787685 Sequence
9	17	100.0	484	2	CS138210	CS138210 Sequence
10	17	100.0	490	2	DD161778	DD161778 COMPOSITI
11	17	100.0	652	2	CQ787683	CQ787683 Sequence
12	17	100.0	652	2	CQ787684	CQ787684 Sequence
13	17	100.0	652	2	CS138208	CS138208 Sequence
14	17	100.0	652	2	CS138209	CS138209 Sequence
15	17	100.0	1190	2	DD161805	DD161805 COMPOSITI
16	17	100.0	1450	2	AX192411	AX192411 Sequence
c 17	17	100.0	1667	1	DQ103854	DQ103854 Unculture
c 18	17	100.0	4418	2	CS124341	CS124341 Sequence
c 19	17	100.0	4418	2	CS124572	CS124572 Sequence
20	17	100.0	4500	2	DD182330	DD182330 CYP2D6 mu
21	17	100.0	5503	5	HUMCYP2DG	M33189 Human debri
c 22	17	100.0	6001	2	CQ806679	CQ806679 Sequence
c 23	17	100.0	6001	2	CQ807053	CQ807053 Sequence
c 24	17	100.0	6001	2	CS124359	CS124359 Sequence
c 25	17	100.0	6001	2	CS124608	CS124608 Sequence
26	17	100.0	6014	5	DQ282157	DQ282157 Homo sapi
27	17	100.0	6018	5	DQ282149	DQ282149 Homo sapi
28	17	100.0	6018	5	DQ282150	DQ282150 Homo sapi
29	17	100.0	6018	5	DQ282155	DQ282155 Homo sapi
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31	17	100.0	6019	5	DQ282151	DQ282151 Homo sapi
32	17	100.0	6019	5	DQ282154	DQ282154 Homo sapi
33	17	100.0	6019	5	DQ282161	DQ282161 Homo sapi
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35	17	100.0	6021	5	DQ282159	DQ282159 Homo sapi
36	17	100.0	6021	5	DQ282160	DQ282160 Homo sapi
37	17	100.0	6026	5	DQ282152	DQ282152 Homo sapi
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46	17	100.0	6376	5	DQ282144	DQ282144 Homo sapi
47	17	100.0	8953	5	AY545216	AY545216 Homo sapi
48	17	100.0	9432	2	AX959041	AX959041 Sequence
49	17	100.0	9432	2	AX394456	AX394456 Sequence
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51	17	100.0	9432	5	HUMCYP2D6	M33388 Human cytoc
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53	17	100.0	13278	5	HSCYP2D7A	X58467 Human CYP2D
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c 62	17	100.0	180421	6	AL805970	AL805970 Mouse DNA
63	17	100.0	202686	6	AL589870	AL589870 Mouse DNA
64	17	100.0	208652	12	BX324228	BX324228 Mus muscu
c 65	17	100.0	211176	12	AC173198	AC173198 Bos tauru
c 66	17	100.0	220629	12	AC095947	AC095947 Rattus no
67	17	100.0	253108	12	AC104517	AC104517 Mus muscu
68	17	100.0	266673	12	AC115671	AC115671 Rattus no
c 69	17	100.0	308565	12	AC163875	AC163875 Bos tauru

ALIGNMENTS

RESULT 1
CS138234
LOCUS CS138234 41 bp DNA linear PAT 17-AUG-2005
DEFINITION Sequence 73 from Patent EP1561823.
ACCESSION CS138234
VERSION CS138234.1 GI:73529673
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Neunaber,R.
TITLE Method for the detection of single nucleotid polymorphisms (SNP) of genes of drug metabolism and test system for performing such a method
JOURNAL Patent: EP 1561823-A 73 10-AUG-2005;
Biotez Berlin-Buch GmbH (DE)

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Qy          1 CGCATCTCCCACCCCCA 17
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Db         24 CGCATCTCCCACCCCCA 40


RESULT 2
AX427056
LOCUS       AX427056                 51 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 20 from Patent WO0196604.
ACCESSION   AX427056
VERSION     AX427056.1  GI:21530439
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bee,G., Kohne,D.E., Korb,L., Peterson,T. and Yguerabide,J.
  TITLE     Assay for genetic polymorphisms using scattered light detectable
            labels
  JOURNAL   Patent: WO 0196604-A 20 20-DEC-2001;
            Genicon Sciences Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db          9 CGCATCTCCCACCCCCA 25


RESULT 3
AX427057
LOCUS       AX427057                 51 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 21 from Patent WO0196604.
ACCESSION   AX427057
VERSION     AX427057.1  GI:21530440
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bee,G., Kohne,D.E., Korb,L., Peterson,T. and Yguerabide,J.
  TITLE     Assay for genetic polymorphisms using scattered light detectable
            labels
  JOURNAL   Patent: WO 0196604-A 21 20-DEC-2001;
            Genicon Sciences Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Exemplary probe for CYP2D6 allele detection"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          9 CGCATCTCCCACCCCCA 25


RESULT 4
CQ815154
LOCUS       CQ815154                 201 bp    DNA     linear   PAT 24-MAY-2004
DEFINITION  Sequence 15 from Patent WO2004033722.
ACCESSION   CQ815154
VERSION     CQ815154.1  GI:47604232
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Roberts,G.W. and Grimaldi,K.
  TITLE     Genetic profiling and healthcare management: adme (absorption,
            distribution, metabolism elimination) toxicology patent application
  JOURNAL   Patent: WO 2004033722-A 15 22-APR-2004;
            Sciona Limited (GB)
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db        181 CGCATCTCCCACCCCCA 197


RESULT 5
CQ815155
LOCUS       CQ815155                 201 bp    DNA     linear   PAT 24-MAY-2004
DEFINITION  Sequence 16 from Patent WO2004033722.
ACCESSION   CQ815155
VERSION     CQ815155.1  GI:47604233
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Roberts,G.W. and Grimaldi,K.
  TITLE     Genetic profiling and healthcare management: adme (absorption,
            distribution, metabolism elimination) toxicology patent application
  JOURNAL   Patent: WO 2004033722-A 16 22-APR-2004;
            Sciona Limited (GB)
FEATURES             Location/Qualifiers
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Qy          1 CGCATCTCCCACCCCCA 17
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Db         84 CGCATCTCCCACCCCCA 100


RESULT 6
CQ787686
LOCUS       CQ787686                483 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 50 from Patent WO2004018707.
ACCESSION   CQ787686
VERSION     CQ787686.1  GI:45722647
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Neunaber,R., Strohner,P., Schreiber,J., Voigt,G. and Schunck,W.H.
  TITLE     Method for identifying single nucleotide polymorphisms (snp) in
            genes which metabolize medicaments and test kit for carrying out
            said method
  JOURNAL   Patent: WO 2004018707-A 50 04-MAR-2004;
            Biotez Berlin-Buch GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .483
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                     /mol_type="unassigned DNA"
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ORIGIN

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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db        265 CGCATCTCCCACCCCCA 281


RESULT 7
CS138211
LOCUS       CS138211                483 bp    DNA     linear   PAT 17-AUG-2005
DEFINITION  Sequence 50 from Patent EP1561823.
ACCESSION   CS138211
VERSION     CS138211.1  GI:73529650
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Neunaber,R.
  TITLE     Method for the detection of single nucleotid polymorphisms (SNP) of
            genes of drug metabolism and test system for performing such a
            method
  JOURNAL   Patent: EP 1561823-A 50 10-AUG-2005;
            Biotez Berlin-Buch GmbH (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db        265 CGCATCTCCCACCCCCA 281


RESULT 8
CQ787685
LOCUS       CQ787685                484 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 49 from Patent WO2004018707.
ACCESSION   CQ787685
VERSION     CQ787685.1  GI:45722646
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Neunaber,R., Strohner,P., Schreiber,J., Voigt,G. and Schunck,W.H.
  TITLE     Method for identifying single nucleotide polymorphisms (snp) in
            genes which metabolize medicaments and test kit for carrying out
            said method
  JOURNAL   Patent: WO 2004018707-A 49 04-MAR-2004;
            Biotez Berlin-Buch GmbH (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db        266 CGCATCTCCCACCCCCA 282


RESULT 9
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LOCUS       CS138210                484 bp    DNA     linear   PAT 17-AUG-2005
DEFINITION  Sequence 49 from Patent EP1561823.
ACCESSION   CS138210
VERSION     CS138210.1  GI:73529649
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Neunaber,R.
  TITLE     Method for the detection of single nucleotid polymorphisms (SNP) of
            genes of drug metabolism and test system for performing such a
            method
  JOURNAL   Patent: EP 1561823-A 49 10-AUG-2005;
            Biotez Berlin-Buch GmbH (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db        266 CGCATCTCCCACCCCCA 282
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RESULT 10
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LOCUS       DD161778                490 bp    DNA     linear   PAT 23-NOV-2005
DEFINITION  COMPOSITIONS AND METHODS FOR INFERRING A RESPONSE TO A STATIN.
ACCESSION   DD161778
VERSION     DD161778.1  GI:83970301
KEYWORDS    JP 2005508612-A/201.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Frudakis,T.
  TITLE     COMPOSITIONS AND METHODS FOR INFERRING A RESPONSE TO A STATIN
  JOURNAL   Patent: JP 2005508612-A 201 07-APR-2005;
            DNAPrint Genomics Inc
COMMENT     OS   Homo sapiens CYP2D6   869777
            PN   JP 2005508612-A/201
            PD   07-APR-2005
            PF   01-JUL-2002 JP 2003509083
            PR   29-JUN-2001 US    60/301867,07-AUG-2001 US    60/310783, PR
            13-SEP-2001 US    60/322478
            PI   tony frudakis
            CC
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
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ORIGIN

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Qy          1 CGCATCTCCCACCCCCA 17
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Db        438 CGCATCTCCCACCCCCA 454


RESULT 11
CQ787683
LOCUS       CQ787683                652 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 47 from Patent WO2004018707.
ACCESSION   CQ787683
VERSION     CQ787683.1  GI:45722644
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Neunaber,R., Strohner,P., Schreiber,J., Voigt,G. and Schunck,W.H.
  TITLE     Method for identifying single nucleotide polymorphisms (snp) in
            genes which metabolize medicaments and test kit for carrying out
            said method
  JOURNAL   Patent: WO 2004018707-A 47 04-MAR-2004;
            Biotez Berlin-Buch GmbH (DE)
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ORIGIN

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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db        298 CGCATCTCCCACCCCCA 314


RESULT 12
CQ787684
LOCUS       CQ787684                652 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 48 from Patent WO2004018707.
ACCESSION   CQ787684
VERSION     CQ787684.1  GI:45722645
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Neunaber,R., Strohner,P., Schreiber,J., Voigt,G. and Schunck,W.H.
  TITLE     Method for identifying single nucleotide polymorphisms (snp) in
            genes which metabolize medicaments and test kit for carrying out
            said method
  JOURNAL   Patent: WO 2004018707-A 48 04-MAR-2004;
            Biotez Berlin-Buch GmbH (DE)
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:32630"
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ORIGIN

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Qy          1 CGCATCTCCCACCCCCA 17
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Db        298 CGCATCTCCCACCCCCA 314


RESULT 13
CS138208
LOCUS       CS138208                652 bp    DNA     linear   PAT 17-AUG-2005
DEFINITION  Sequence 47 from Patent EP1561823.
ACCESSION   CS138208
VERSION     CS138208.1  GI:73529647
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Neunaber,R.
  TITLE     Method for the detection of single nucleotid polymorphisms (SNP) of
            genes of drug metabolism and test system for performing such a
            method
  JOURNAL   Patent: EP 1561823-A 47 10-AUG-2005;
            Biotez Berlin-Buch GmbH (DE)
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        298 CGCATCTCCCACCCCCA 314


RESULT 14
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CS138209
LOCUS       CS138209                652 bp    DNA     linear   PAT 17-AUG-2005
DEFINITION  Sequence 48 from Patent EP1561823.
ACCESSION   CS138209
VERSION     CS138209.1  GI:73529648
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Neunaber,R.
  TITLE     Method for the detection of single nucleotid polymorphisms (SNP) of
            genes of drug metabolism and test system for performing such a
            method
  JOURNAL   Patent: EP 1561823-A 48 10-AUG-2005;
            Biotez Berlin-Buch GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .652
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match           100.0%;  Score 17;  DB 2;  Length 652;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        298 CGCATCTCCCACCCCCA 314


RESULT 15
DD161805
LOCUS       DD161805                1190 bp    DNA     linear   PAT 23-NOV-2005
DEFINITION  COMPOSITIONS AND METHODS FOR INFERRING A RESPONSE TO A STATIN.
ACCESSION   DD161805
VERSION     DD161805.1  GI:83970328
KEYWORDS    JP 2005508612-A/228.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1190)
  AUTHORS   Frudakis,T.
  TITLE     COMPOSITIONS AND METHODS FOR INFERRING A RESPONSE TO A STATIN
  JOURNAL   Patent: JP 2005508612-A 228 07-APR-2005;
            DNAPrint Genomics Inc
COMMENT     OS   Homo sapiens CYP2D6   756251
            PN   JP 2005508612-A/228
            PD   07-APR-2005
            PF   01-JUL-2002 JP 2003509083
            PR   29-JUN-2001 US    60/301867,07-AUG-2001 US    60/310783, PR
            13-SEP-2001 US    60/322478
            PI   tony frudakis
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1190
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match           100.0%;  Score 17;  DB 2;  Length 1190;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        438 CGCATCTCCCACCCCCA 454


RESULT 16
AX192411
LOCUS       AX192411                1450 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 1 from Patent WO0149883.
ACCESSION   AX192411
VERSION     AX192411.1  GI:15210375
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Katz,D.A., Gentile-Davey,M.C., Cornwell,M.J. and Huff,J.B.
  TITLE     Amplification based polymorphism detection
  JOURNAL   Patent: WO 0149883-A 1 12-JUL-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .1450
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 17;  DB 2;  Length 1450;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        298 CGCATCTCCCACCCCCA 314


RESULT 17
DQ103854/c
LOCUS       DQ103854                1667 bp    DNA     linear   ENV 25-JAN-2006
DEFINITION  Uncultured marine eukaryote clone M2_18B02 small subunit ribosomal
            RNA gene, partial sequence.
ACCESSION   DQ103854
VERSION     DQ103854.1  GI:73533451
KEYWORDS    ENV.
SOURCE      uncultured marine eukaryote
  ORGANISM  uncultured marine eukaryote
            Eukaryota; environmental samples.
REFERENCE   1  (bases 1 to 1667)
  AUTHORS   Zuendorf,A., Behnke,A., Bunge,J., Barger,K. and Stoeck,T.
  TITLE     Diversity Estimates of Microeukaryotes below the Chemocline of the
            Anoxic Mariager Fjord, Denmark
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1667)
  AUTHORS   Zuendorf,A., Behnke,A., Bunge,J., Barger,K. and Stoeck,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2005) Biology/Ecology, TU Kaiserslautern, Erwin
            Schrodinger Str. 14, Kaiserslautern 67663, Germany
FEATURES             Location/Qualifiers
     source          1. .1667
                     /organism="uncultured marine eukaryote"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:203449"
                     /clone="M2_18B02"
                     /environmental_sample
     rRNA            <1. .>1667
                     /product="small subunit ribosomal RNA"
ORIGIN

  Query Match           100.0%;  Score 17;  DB 1;  Length 1667;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        661 CGCATCTCCCACCCCCA 645
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RESULT 18
CS124341/c
LOCUS       CS124341                4418 bp    DNA     linear   PAT 21-JUL-2005
DEFINITION  Sequence 27 from Patent WO2005059172.
ACCESSION   CS124341
VERSION     CS124341.1  GI:71057406
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Foekens,J.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2005059172-A 27 30-JUN-2005;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .4418
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 4418;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       2147 CGCATCTCCCACCCCCA 2131


RESULT 19
CS124572/c
LOCUS       CS124572                4418 bp    DNA     linear   PAT 21-JUL-2005
DEFINITION  Sequence 258 from Patent WO2005059172.
ACCESSION   CS124572
VERSION     CS124572.1  GI:71057727
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Foekens,J.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2005059172-A 258 30-JUN-2005;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .4418
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 4418;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       2147 CGCATCTCCCACCCCCA 2131


RESULT 20
DD182330
LOCUS       DD182330                4500 bp    DNA     linear   PAT 19-JAN-2006
DEFINITION  CYP2D6 mutated gene.
ACCESSION   DD182330
VERSION     DD182330.1  GI:85656896
KEYWORDS    JP 2005176601-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 4500)
  AUTHORS   Tsuchiya,N., Taniyama,M., Ogawa,K. and Hibino,T.
  TITLE     CYP2D6 mutated gene
  JOURNAL   Patent: JP 2005176601-A 1 07-JUL-2005;
            Tsumura Inc
COMMENT     OS   Human
            PN   JP 2005176601-A/1
            PD   07-JUL-2005
            PF   06-DEC-2001 JP 2001372548
            PI   naoko tsuchiya,mitsue taniyama,kazuo ogawa,tomoko hibino CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .4500
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 4500;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       1829 CGCATCTCCCACCCCCA 1845


RESULT 21
HUMCYP2DG
LOCUS       HUMCYP2DG               5503 bp    DNA     linear   PRI 27-APR-1993
DEFINITION  Human debrisoquine 4-hydroxylase mutant allele (CYP2D6-MA1) gene,
            complete cds.
ACCESSION   M33189
VERSION     M33189.1  GI:181305
KEYWORDS    debrisoquine 4-hydroxylase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 5503)
  AUTHORS   Gonzalez,F.J.
  JOURNAL   Unpublished (1990)
COMMENT     Original source text: Human individual MAGA DNA.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by F.Gonzalez, 23-MAR-1990, for release after publication.
               Author address: F.Gonzalez
               National Cancer Institute
               Bldg. 37 Rm. 3E-24
               National Institute of Health
               Bethesda, Md 20892.
FEATURES             Location/Qualifiers
     source          1. .5503
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     TATA_signal     689. .702
     prim_transcript 726. .5103
                     /note="debrisoquine 4-hydroxylase mRNA and introns"
     CDS             join(814. .993,1696. .1877,2419. .2571,2661. .2820,3254. .3430,
                     3621. .3762,3970. .4157,4612. .4753,4852. .5030)
                     /note="debrisoquine 4-hydroxylase"
                     /codon_start=1
                     /protein_id="AAA35737.1"
                     /db_xref="GI:181306"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYSPGPLPLPGLG
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                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREAMVTRGEDTADRP
                     PVPITQILGFGPRSQGKQRGVPGALWARVARAEALLRLHLAQLGPGQEVAGAVGDRGG
                     RLPLCRLRQPLRRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKE
                     ESGFLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTE
                     AFLAEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRV
                     QQEIDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRI
                     PKGTTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEP
                     LARMELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
     exon            <814. .993
                     /note="debrisoquine 4-hydroxylase"
                     /number=1
     intron          994. .1695
                     /note="debrisoquine 4-hydroxylase intron A"
     exon            1696. .1877
                     /number=2
     intron          1878. .2418
                     /note="debrisoquine 4-hydroxylase intron B"
     exon            2419. .2571
                     /number=3
     intron          2572. .2660
                     /note="debrisoquine 4-hydroxylase intron C"
     exon            2661. .2820
                     /number=4
     intron          2821. .3253
                     /note="debrisoquine 4-hydroxylase intron D"
     exon            3254. .3430
                     /number=5
     intron          3431. .3620
                     /note="debrisoquine 4-hydroxylase intron E"
     exon            3621. .3762
                     /number=6
     intron          3763. .3969
                     /note="debrisoquine 4-hydroxylase intron F"
     exon            3970. .4157
                     /number=7
     intron          4158. .4611
                     /note="debrisoquine 4-hydroxylase intron G"
     exon            4612. .4753
                     /number=8
     intron          4754. .4851
                     /note="debrisoquine 4-hydroxylase intron H"
     exon            4852. .>5030
                     /note="debrisoquine 4-hydroxylase"
                     /number=9
ORIGIN      Chromosome 22.

  Query Match            100.0%;  Score 17;  DB 5;  Length 5503;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       2642 CGCATCTCCCACCCCCA 2658


RESULT 22
CQ806679/c
LOCUS       CQ806679               6001 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 129 from Patent WO2004035803.
ACCESSION   CQ806679
VERSION     CQ806679.1  GI:47112061
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
            Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
            Marx,A.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2004035803-A 129 29-APR-2004;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .6001
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            100.0%;  Score 17;  DB 2;  Length 6001;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3105 CGCATCTCCCACCCCCA 3089


RESULT 23
CQ807053/c
LOCUS       CQ807053               6001 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 503 from Patent WO2004035803.
ACCESSION   CQ807053
VERSION     CQ807053.1  GI:47112435
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
            Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
            Marx,A.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2004035803-A 503 29-APR-2004;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .6001
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match            100.0%;  Score 17;  DB 2;  Length 6001;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3105 CGCATCTCCCACCCCCA 3089


RESULT 24
CS124359/c
LOCUS       CS124359               6001 bp    DNA     linear   PAT 21-JUL-2005
DEFINITION  Sequence 45 from Patent WO2005059172.
ACCESSION   CS124359
VERSION     CS124359.1  GI:71057424
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Foekens,J.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2005059172-A 45 30-JUN-2005;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .6001
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 6001;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3105 CGCATCTCCCACCCCCA 3089


RESULT 25
CS124608/c
LOCUS       CS124608                6001 bp    DNA     linear   PAT 21-JUL-2005
DEFINITION  Sequence 294 from Patent WO2005059172.
ACCESSION   CS124608
VERSION     CS124608.1  GI:71057763
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Foekens,J.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2005059172-A 294 30-JUN-2005;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .6001
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 6001;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3105 CGCATCTCCCACCCCCA 3089


RESULT 26
DQ282157
LOCUS       DQ282157                6014 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*17 allele,
            complete cds.
ACCESSION   DQ282157
VERSION     DQ282157.1  GI:82492099
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6014)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6014)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6014
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     variation       23
                     /note="compared to NG_003180"
                     /replace="c"
     variation       929
                     /note="compared to NG_003180"
                     /replace="g"
     gene            1519. .5897
                     /gene="CYP2D6"
                     /allele="CYP2D6*17"
     mRNA            join(1519. .1786,2489. .2660,3213. .3365,3454. .3614,
                     4048. .4224,4415. .4556,4764. .4951,5406. .5547,5646. .5897)
                     /gene="CYP2D6"
                     /allele="CYP2D6*17"
     CDS             join(1607. .1786,2489. .2660,3213. .3365,3454. .3614,
                     4048. .4224,4415. .4556,4764. .4951,5406. .5547,5646. .5824)
                     /gene="CYP2D6"
                     /allele="CYP2D6*17"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77905.1"
                     /db_xref="GI:82492100"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPIIQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLCIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
     variation       2259
                     /gene="CYP2D6"
                     /note="compared to NG_003180"
                     /replace="t"
     variation       2351
                     /gene="CYP2D6"
                     /note="compared to NG_003180"
                     /replace="c"
     variation       2628
                     /gene="CYP2D6"
                     /note="compared to NG_003180"
                     /replace="t"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6014;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3436 CGCATCTCCCACCCCCA 3452


RESULT 27
DQ282149
LOCUS       DQ282149                6018 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens nonfunctional cytochrome P450 2D6 (CYP2D6) gene,
            CYP2D6*4A allele, complete sequence.
ACCESSION   DQ282149
VERSION     DQ282149.1  GI:82492085
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6018)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
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  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6018)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6018
                     /organism="Homo sapiens"
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                     Number  AY545216"
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     variation       371
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                     Number  AY545216"
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     variation       606
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                     Number  AY545216"
                     /replace="a"
     gene            1518. .5896
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                     /allele="CYP2D6*4A"
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                     /allele="CYP2D6*4A"
                     /note="nonfunctional cytochrome P450 2D6 due to mutation"
     variation       1705
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
     variation       1915
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       2350
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                     Number  AY545216"
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       2578
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       2588
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       3452
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       3703
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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                     Number  AY545216"
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     variation       5188
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                     Number  AY545216"
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6018;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3435 CGCATCTCCCACCCCCA 3451


RESULT 28
DQ282150
LOCUS       DQ282150                6018 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens nonfunctional cytochrome P450 2D6 (CYP2D6) gene,
            CYP2D6*4D allele, complete sequence.
ACCESSION   DQ282150
VERSION     DQ282150.1  GI:82492086
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6018)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6018)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6018
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                Number  AY545216"
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                /gene="CYP2D6"
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                4048. .4224,4415. .4556,4764. .4951,5406. .5547,5646. .5897)
                /gene="CYP2D6"
                /allele="CYP2D6*4D"
     misc_feature join(1607. .1786,2489. .2660,3213. .3365,3454. .3614,
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                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="t"
     variation  2448
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                Number  AY545216"
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                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
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     variation  3268
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                Number  AY545216"
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                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
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                Number  AY545216"
                /replace="c"
     variation  5000
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
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     variation  5189
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6018;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3436 CGCATCTCCCACCCCCA 3452


RESULT 29
DQ282155
LOCUS       DQ282155               6018 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*45B allele,
            complete cds.
ACCESSION   DQ282155
VERSION     DQ282155.1  GI:82492095
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6018)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6018)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6018
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                     Number  AY545216"
                     /replace="a"
     variation       379
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                     Number  AY545216"
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     variation       874
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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                     4051. .4227,4418. .4559,4767. .4954,5409. .5550,5649. .5900)
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     CDS             join(1610. .1789,2492. .2663,3216. .3368,3457. .3617,
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                /db_xref="GI:82492096"
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                CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
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                TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
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variation       1919
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                /replace="g"
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                /replace="g"
variation       3271
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                /note="compared to CYP2D6*1 allele of GenBank Accession
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variation       3326
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                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
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variation       4185
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                /note="compared to CYP2D6*1 allele of GenBank Accession
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                Number  AY545216"
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6018;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3439 CGCATCTCCCACCCCCA 3455


RESULT 30
DQ282158
LOCUS       DQ282158               6018 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*17V allele,
            complete cds.
ACCESSION   DQ282158
VERSION     DQ282158.1  GI:82492101
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6018)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6018)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6018
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                     /db_xref="taxon:9606"
     variation       16
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     variation       924
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                     4043. .4219,4410. .4551,4759. .4946,5401. .5542,5641. .5892)
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                     /allele="CYP2D6*17V"
     CDS             join(1602. .1781,2484. .2655,3208. .3360,3449. .3609,
                     4043. .4219,4410. .4551,4759. .4946,5401. .5542,5641. .5819)
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                     /allele="CYP2D6*17V"
                     /codon_start=1
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                     /db_xref="GI:82492102"
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                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
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                     AEMEKAKGNPESSFNDENLCIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3431 CGCATCTCCCACCCCCA 3447


RESULT 31
DQ282151
LOCUS       DQ282151                6019 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*9 allele,
            complete cds.
ACCESSION   DQ282151
VERSION     DQ282151.1  GI:82492087
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6019)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6019)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6019
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     gene            1522. .5897
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     CDS             join(1610. .1789,2492. .2663,3216. .3368,3457. .3617,
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                     /gene="CYP2D6"
                     /allele="CYP2D6*9"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77899.1"
                     /db_xref="GI:82492088"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQEI
                     DDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKGT
                     TLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLARM
                     ELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVSPSPYELCAVPR"
     variation       4222^4223
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6019;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3439 CGCATCTCCCACCCCCA 3455


RESULT 32
DQ282154
LOCUS       DQ282154                6019 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*43 allele,
            complete cds.
ACCESSION   DQ282154
VERSION     DQ282154.1  GI:82492093
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6019)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6019)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6019
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1519. .5897
                     /gene="CYP2D6"
                     /allele="CYP2D6*43"
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                     4048. .4224,4415. .4556,4764. .4951,5406. .5547,5646. .5897)
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                     4048. .4224,4415. .4556,4764. .4951,5406. .5547,5646. .5824)
                     /gene="CYP2D6"
                     /allele="CYP2D6*43"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77902.1"
                     /db_xref="GI:82492094"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRHQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
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                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVSPSPYELCAVPR"
     variation       1683
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="a"
     variation       1916
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6019;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3436 CGCATCTCCCACCCCCA 3452


RESULT 33
DQ282161
LOCUS       DQ282161               6019 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens nonfunctional cytochrome P450 2D6 (CYP2D6) gene,
            CYP2D6*56 allele, complete sequence.
ACCESSION   DQ282161
VERSION     DQ282161.1  GI:82492107
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6019)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6019)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6019
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                     /db_xref="taxon:9606"
     gene            1519. .5897
                     /gene="CYP2D6"
                     /allele="CYP2D6*56"
     mRNA            join(1519. .1786,2489. .2660,3213. .3365,3454. .3614,
                     4048. .4224,4415. .4556,4764. .4951,5406. .5547,5646. .5897)
                     /gene="CYP2D6"
                     /allele="CYP2D6*56"
     misc_feature    join(1607. .1786,2489. .2660,3213. .3365,3454. .3614,
                     4048. .4224,4415. .4556,4764. .4951,5406. .5547,5646. .5824)
                     /gene="CYP2D6"
                     /allele="CYP2D6*56"
                     /note="nonfunctional cytochrome P450 2D6 due to mutation"
     variation       4808
                     /gene="CYP2D6"
                     /note="compared to NG_003180"
                     /replace="t"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6019;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3436 CGCATCTCCCACCCCCA 3452


RESULT 34
DQ282148
LOCUS       DQ282148               6021 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens nonfunctional cytochrome P450 2D6 (CYP2D6) gene,
            CYP2D6*3 allele, complete sequence.
ACCESSION   DQ282148
VERSION     DQ282148.1  GI:82492084
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6021)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6021)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6021
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1522. .5899
                     /gene="CYP2D6"
                     /allele="CYP2D6*3"
     mRNA            join(1522. .1789,2492. .2663,3216. .3368,3457. .3617,
                     4051. .4226,4417. .4558,4766. .4953,5408. .5549,5648. .5899)
                     /gene="CYP2D6"
                     /allele="CYP2D6*3"
     misc_feature    join(1610. .1789,2492. .2663,3216. .3368,3457. .3617,
                     4051. .4226,4417. .4558,4766. .4953,5408. .5549,5648. .5826)
                     /gene="CYP2D6"
                     /allele="CYP2D6*3"
                     /note="nonfunctional cytochrome P450 2D6 due to mutation"
     variation       4158^4159
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="a"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6021;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3439 CGCATCTCCCACCCCCA 3455


RESULT 35
DQ282159
LOCUS       DQ282159               6021 bp    DNA     linear   PRI 22-NOV-2005
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DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*35 allele,
            complete cds.
ACCESSION   DQ282159
VERSION     DQ282159.1  GI:82492103
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6021)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6021)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6021
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1525. .5903
                     /gene="CYP2D6"
                     /allele="CYP2D6*35"
     mRNA            join(1525. .1792,2495. .2666,3219. .3371,3460. .3620,
                     4054. .4230,4421. .4562,4770. .4957,5412. .5553,5652. .5903)
                     /gene="CYP2D6"
                     /allele="CYP2D6*35"
     CDS             join(1613. .1792,2495. .2666,3219. .3371,3460. .3620,
                     4054. .4230,4421. .4562,4770. .4957,5412. .5553,5652. .5830)
                     /gene="CYP2D6"
                     /allele="CYP2D6*35"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77907.1"
                     /db_xref="GI:82492104"
                     /translation="MGLEALVPLAMIVAIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLCIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
     variation       1643
                     /gene="CYP2D6"
                     /note="compared to NG_003180"
                     /replace="a"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6021;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3442 CGCATCTCCCACCCCCA 3458


RESULT 36
DQ282160
LOCUS       DQ282160               6021 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*41 allele,
            complete cds.
ACCESSION   DQ282160
VERSION     DQ282160.1  GI:82492105
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6021)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6021)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6021
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                     /db_xref="taxon:9606"
     variation       26
                     /note="compared to NG_003180"
                     /replace="c"
     gene            1525. .5903
                     /gene="CYP2D6"
                     /allele="CYP2D6*41"
     mRNA            join(1525. .1792,2495. .2666,3219. .3371,3460. .3620,
                     4054. .4230,4421. .4562,4770. .4957,5412. .5553,5652. .5903)
                     /gene="CYP2D6"
                     /allele="CYP2D6*41"
     CDS             join(1613. .1792,2495. .2666,3219. .3371,3460. .3620,
                     4054. .4230,4421. .4562,4770. .4957,5412. .5553,5652. .5830)
                     /gene="CYP2D6"
                     /allele="CYP2D6*41"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77908.1"
                     /db_xref="GI:82492106"
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                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLCIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6021;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3442 CGCATCTCCCACCCCCA 3458


RESULT 37
DQ282152
LOCUS       DQ282152               6026 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*10B allele,
            complete cds.
ACCESSION   DQ282152
VERSION     DQ282152.1  GI:82492089
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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          Hominidae; Homo.
REFERENCE   1  (bases 1 to 6026)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6026)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     Number  AY545216"
                     /replace="t"
     variation       375
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="g"
     variation       610
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="a"
     gene            1522. .5900
                     /gene="CYP2D6"
                     /allele="CYP2D6*10B"
     mRNA            join(1522. .1789,2492. .2663,3216. .3368,3457. .3617,
                     4051. .4227,4418. .4559,4767. .4954,5409. .5550,5649. .5900)
                     /gene="CYP2D6"
                     /allele="CYP2D6*10B"
     CDS             join(1610. .1789,2492. .2663,3216. .3368,3457. .3617,
                     4051. .4227,4418. .4559,4767..4954,5409. .5550,5649. .5827)
                     /gene="CYP2D6"
                     /allele="CYP2D6*10B"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77900.1"
                     /db_xref="GI:82492090"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYSPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
     variation       1709
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
     variation       1919
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
     variation       2451
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="g"
     variation       2647
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
     variation       3271
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       3707
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                     Number  AY545216"
                     /replace="g"
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                     Number  AY545216"
                     /replace="c"
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="g"
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3439 CGCATCTCCCACCCCCA 3455


RESULT 38
DQ282162
LOCUS       DQ282162               6029 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*58 allele,
            complete cds.
ACCESSION   DQ282162
VERSION     DQ282162.1  GI:82492108
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6029)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6029)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6029
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     variation       26
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     variation       934
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                     /replace="g"
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                     /allele="CYP2D6*58"
     mRNA            join(1524. .1791,2494. .2665,3218. .3370,3459. .3628,
                     4062. .4238,4429. .4570,4778. .4965,5420. .5561,5660. .5911)
                     /gene="CYP2D6"
                     /allele="CYP2D6*58"
     CDS             join(1612. .1791,2494. .2665,3218. .3370,3459. .3628,
                     4062. .4238,4429. .4570,4778. .4965,5420. .5561,5660. .5838)
                     /gene="CYP2D6"
                     /allele="CYP2D6*58"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77909.1"
                     /db_xref="GI:82492109"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPIIQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKE
                     ESGFLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTE
                     AFLAEMEKAKGNPESSFNDENLCIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRV
                     QQEIDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRI
                     PKGTTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEP
                     LARMELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
     variation       2356
                     /gene="CYP2D6"
                     /note="compared to NG_003180"
                     /replace="c"
     variation       2633
                     /gene="CYP2D6"
                     /note="compared to NG_003180"
                     /replace="t"
     variation       3476. .3484
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                     /note="compared to NG_003180"
                     /replace=""
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6029;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3441 CGCATCTCCCACCCCCA 3457


RESULT 39
DQ282145
LOCUS       DQ282145                6321 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*1_AA allele,
            complete cds.
ACCESSION   DQ282145
VERSION     DQ282145.1  GI:82492078
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6321)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6321)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6321
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="African American"
     gene            1522. .5901
                     /gene="CYP2D6"
                     /allele="CYP2D6*1_AA"
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                     4052. .4228,4419. .4560,4768. .4955,5410. .5551,5650. .5901)
                     /gene="CYP2D6"
                     /allele="CYP2D6*1_AA"
     variation       1567
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace=""
     CDS             join(1611. .1790,2493. .2664,3217. .3369,3458. .3618,
                     4052. .4228,4419. .4560,4768. .4955,5410. .5551,5650. .5828)
                     /gene="CYP2D6"
                     /allele="CYP2D6*1_AA"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77896.1"
                     /db_xref="GI:82492079"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6321;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3440 CGCATCTCCCACCCCCA 3456


RESULT 40
DQ282163
LOCUS       DQ282163                6355 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Pan paniscus cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*Bonobo
            allele, complete cds.
ACCESSION   DQ282163
VERSION     DQ282163.1  GI:82492110
KEYWORDS    .
SOURCE      Pan paniscus (pygmy chimpanzee)
  ORGANISM  Pan paniscus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 6355)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6355)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6355
                     /organism="Pan paniscus"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9597"
     gene            1507. .5883
                     /gene="CYP2D6"
                     /allele="CYP2D6*Bonobo"
     mRNA            join(1507. .1774,2477. .2648,3199. .3351,3439. .3599,
                     4033. .4209,4400. .4541,4749. .4936,5392. .5533,5632. .5883)
                     /gene="CYP2D6"
                     /allele="CYP2D6*Bonobo"
     CDS             join(1595. .1774,2477. .2648,3199. .3351,3439. .3599,
                     4033. .4209,4400. .4541,4749. .4936,5392. .5533,5632. .5810)
                     /gene="CYP2D6"
                     /allele="CYP2D6*Bonobo"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77910.1"
                     /db_xref="GI:82492111"
                     /translation="MGLEALVPLAVIVTIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQARMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLFTNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6355;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3421 CGCATCTCCCACCCCCA 3437


RESULT 41
DQ282164
LOCUS       DQ282164               6368 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Pan troglodytes cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*Chimp
            allele, complete cds.
ACCESSION   DQ282164
VERSION     DQ282164.1  GI:82492112
KEYWORDS    .
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 6368)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6368)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6368
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            1518. .5896
                     /gene="CYP2D6"
                     /allele="CYP2D6*Chimp"
     mRNA            join(1518. .1785,2487. .2658,3211. .3363,3452. .3612,
                     4046. .4222,4413. .4554,4762. .4949,5405. .5546,5645. .5896)
                     /gene="CYP2D6"
                     /allele="CYP2D6*Chimp"
     CDS             join(1606. .1785,2487. .2658,3211. .3363,3452. .3612,
                     4046. .4222,4413. .4554,4762. .4949,5405. .5546,5645. .5823)
                     /gene="CYP2D6"
                     /allele="CYP2D6*Chimp"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77911.1"
                     /db_xref="GI:82492113"
                     /translation="MGLEALVPLAVIVTIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAIPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGIVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQARMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLFTNLSSVLKDKAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6368;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3434 CGCATCTCCCACCCCCA 3450


RESULT 42
DQ282153
LOCUS       DQ282153               6371 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*29 allele,
            complete cds.
ACCESSION   DQ282153
VERSION     DQ282153.1  GI:82492091
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6371)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6371)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6371
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     variation       16
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                     Number  AY545216"
                     /replace="c"
     variation       192
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="a"
     variation       202
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="a"
     variation       375
                     /note="compared to CYP2D6*1 allele of GenBank Accession
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                Number  AY545216"
                /replace="g"
     variation  870
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="t"
     variation  1434
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="a"
     gene       1522. .5899
                /gene="CYP2D6"
                /allele="CYP2D6*29"
     mRNA       join(1522. .1789,2491. .2662,3215. .3367,3456. .3616,
                4050. .4226,4417. .4558,4766. .4953,5408. .5549,5648. .5899)
                /gene="CYP2D6"
                /allele="CYP2D6*29"
     CDS        join(1610. .1789,2491. .2662,3215. .3367,3456. .3616,
                4050. .4226,4417. .4558,4766. .4953,5408. .5549,5648. .5826)
                /gene="CYP2D6"
                /allele="CYP2D6*29"
                /codon_start=1
                /product="cytochrome P450 2D6"
                /protein_id="ABB77901.1"
                /db_xref="GI:82492092"
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                NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                PVPITQILGFGPRSQGVFLARYGPAWREQRRFSISTLRNLGLGKKSLEQWVTEEAACL
                CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                AEMEKAKGNPESSFNDENLCIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                IDDMIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
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     variation  1919
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                /note="compared to CYP2D6*1 allele of GenBank Accession
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                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="c"
     variation  2353
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                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="g"
     variation  2450
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="g"
     variation  3268
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
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     variation  3270
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="c"
     variation  3732
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="t"
     variation  3824
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="g"
     variation  3901
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="a"
     variation  4459
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
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     variation  4792
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="a"
     variation  4993
                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="c"
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                /gene="CYP2D6"
                /note="compared to CYP2D6*1 allele of GenBank Accession
                Number  AY545216"
                /replace="c"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6371;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3438 CGCATCTCCCACCCCCA 3454


RESULT 43
DQ282146
LOCUS       DQ282146               6372 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*1V_AA
            allele, complete cds.
ACCESSION   DQ282146
VERSION     DQ282146.1  GI:82492080
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6372)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6372)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6372
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="African American"
     gene            1522. .5900
                     /gene="CYP2D6"
                     /allele="CYP2D6*1V_AA"
     mRNA            join(1522. .1789,2492. .2663,3216. .3368,3457. .3617,
                     4051. .4227,4418. .4559,4767. .4954,5409. .5550,5649. .5900)
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                     /allele="CYP2D6*1V_AA"
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                     4051. .4227,4418. .4559,4767. .4954,5409. .5550,5649. .5827)
                     /gene="CYP2D6"
                     /allele="CYP2D6*1V_AA"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77897.1"
                     /db_xref="GI:82492081"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVSPSPYELCAVPR"
     variation       1919
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
     variation       2451
                     /gene="CYP2D6"
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="g"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6372;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3439 CGCATCTCCCACCCCCA 3455


RESULT 44
DQ282147
LOCUS       DQ282147               6374 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*2L allele,
            complete cds.
ACCESSION   DQ282147
VERSION     DQ282147.1  GI:82492082
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6374)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6374)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6374
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
     variation       312
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                     Number  AY545216"
                     /replace="a"
     variation       377
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="g"
     variation       872
                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
     gene            1524. .5902
                     /gene="CYP2D6"
                     /allele="CYP2D6*2L"
     mRNA            join(1524. .1791,2494. .2665,3218. .3370,3459. .3619,
                     4053. .4229,4420. .4561,4769. .4956,5411. .5552,5651. .5902)
                     /gene="CYP2D6"
                     /allele="CYP2D6*2L"
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                     4053. .4229,4420. .4561,4769. .4956,5411. .5552,5651. .5829)
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                     /protein_id="ABB77898.1"
                     /db_xref="GI:82492083"
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                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
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                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
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     variation       1921
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     variation       2356
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       2453
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="g"
     variation       3273
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="c"
     variation       4462
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
     variation       4996
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       5196
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
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     variation       5402
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                     /note="compared to CYP2D6*1 allele of GenBank Accession
                     Number  AY545216"
                     /replace="t"
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     variation       5792
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6374;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3441 CGCATCTCCCACCCCCA 3457


RESULT 45
DQ282156
LOCUS       DQ282156               6374 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*2D allele,
            complete cds.
ACCESSION   DQ282156
VERSION     DQ282156.1  GI:82492097
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6374)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6374)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
     source          1. .6374
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1524. .5902
                     /gene="CYP2D6"
                     /allele="CYP2D6*2D"
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                     4053. .4229,4420. .4561,4769. .4956,5411. .5552,5651. .5902)
                     /gene="CYP2D6"
                     /allele="CYP2D6*2D"
     CDS             join(1612. .1791,2494. .2665,3218. .3370,3459. .3619,
                     4053. .4229,4420. .4561,4769. .4956,5411. .5552,5651. .5829)
                     /gene="CYP2D6"
                     /allele="CYP2D6*2D"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB77904.1"
                     /db_xref="GI:82492098"
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                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLCIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
     variation       3273
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6374;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3441 CGCATCTCCCACCCCCA 3457


RESULT 46
DQ282144
LOCUS       DQ282144               6376 bp    DNA     linear   PRI 22-NOV-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*1V allele,
            complete cds.
ACCESSION   DQ282144
VERSION     DQ282144.1  GI:82492076
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 6376)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     CYP2D6 Evolution and Allele Diversity Among Human Races
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6376)
  AUTHORS   Koch,W.H., Nikoloff,D.M., Lu,W., Pan,R.M., deLeon,J. and
            Wedlund,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-2005) College of Pharmacy, University of
            Kentucky, 420 College of Pharmacy Building, Lexington, KT
            40536-0082, USA
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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                     /gene="CYP2D6"
                     /allele="CYP2D6*1V"
     mRNA            join(<1614. .1793,2496. .2667,3220. .3372,3461. .3621,
                     4055. .4231,4422. .4563,4771. .4958,5413. .5554,5653. .>5831)
                     /gene="CYP2D6"
                     /allele="CYP2D6*1V"
                     /product="cytochrome P450 2D6"
     CDS             join(1614. .1793,2496. .2667,3220. .3372,3461. .3621,
                     4055. .4231,4422. .4563,4771. .4958,5413. .5554,5653. .5831)
                     /gene="CYP2D6"
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                     /codon_start=1
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                     /protein_id="ABB77895.1"
                     /db_xref="GI:82492077"
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                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
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     variation       2455
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     variation       2782
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 6376;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3443 CGCATCTCCCACCCCCA 3459


RESULT 47
AY545216
LOCUS       AY545216               8953 bp    DNA     linear   PRI 17-OCT-2005
DEFINITION  Homo sapiens cytochrome P4502D6 (CYP2D6) gene, CYP2D6*1 allele,
            complete cds.
ACCESSION   AY545216
VERSION     AY545216.1  GI:45024927
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 8953)
  AUTHORS   Gaedigk,A., Bhathena,A., Ndjountche,L., Pearce,R.E.,
            Abdel-Rahman,S.M., Alander,S.W., Bradford,L.D., Rogan,P.K. and
            Leeder,J.S.
  TITLE     Identification and characterization of novel sequence variations in
            the cytochrome P4502D6 (CYP2D6) gene in African Americans
  JOURNAL   Pharmacogenomics J. 5 (3), 173-182 (2005)
   PUBMED   15768052
REFERENCE   2  (bases 1 to 8953)
  AUTHORS   Gaedigk,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-2004) Section of Developmental Pharmacology &
            Experimental Therapeutics, Children's Mercy Hospital & Clinics,
            2401 Gillham Rd, Kansas City, MO 64108, USA
FEATURES             Location/Qualifiers
     source          1. .8953
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /pop_variant="caucasian"
     gene            4113. .8491
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                     /allele="CYP2D6*1"
     mRNA            join(4113. .4380,5083. .5254,5807. .5959,6048. .6208,
                     6642. .6818,7009. .7150,7358. .7545,8000. .8141,8240. .8491)
                     /gene="CYP2D6"
                     /allele="CYP2D6*1"
                     /product="cytochrome P4502D6"
     CDS             join(4201. .4380,5083. .5254,5807. .5959,6048. .6208,
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                     /allele="CYP2D6*1"
                     /codon_start=1
                     /product="cytochrome P4502D6"
                     /protein_id="AAS55001.1"
                     /db_xref="GI:45024928"
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                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
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ORIGIN

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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       6030 CGCATCTCCCACCCCCA 6046


RESULT 48
AX959041
LOCUS       AX959041               9432 bp    DNA     linear   PAT 14-JAN-2004
DEFINITION  Sequence 50 from Patent WO03100091.
ACCESSION   AX959041
VERSION     AX959041.1  GI:40879771
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Brockmoeller,H.J.
  TITLE     Means and methods for improved treatment using setrones
  JOURNAL   Patent: WO 03100091-A 50 04-DEC-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .9432
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 49
AX394456
LOCUS       AX394456               9432 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 1 from Patent WO0218638.
ACCESSION   AX394456
VERSION     AX394456.1  GI:21065594
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
  TITLE     Detection of cyp2d6 polymorphisms
  JOURNAL   Patent: WO 0218638-A 1 07-MAR-2002;
            Gemini Genomics PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .9432
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CGCATCTCCCACCCCCA 17
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Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 50
AX687027
LOCUS       AX687027               9432 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1 from Patent EP1281755.
ACCESSION   AX687027
VERSION     AX687027.1  GI:29409531
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Milos,P.M. and Webb,S.M.
  TITLE     Variants of the human cyp2d6 gene
  JOURNAL   Patent: EP 1281755-A 1 05-FEB-2003;
            Pfizer Products Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9432
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 51
HUMCYP2D6
LOCUS       HUMCYP2D6              9432 bp    DNA     linear   PRI 22-NOV-1994
DEFINITION  Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
ACCESSION   M33388
VERSION     M33388.1  GI:181303
KEYWORDS    cytochrome P450; cytochrome P450 IID6.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 9432)
  AUTHORS   Kimura,S., Umeno,M., Skoda,R.C., Meyer,U.A. and Gonzalez,F.J.
  TITLE     The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and
            identification of the polymorphic CYP2D6 gene, a related gene, and
            a pseudogene
  JOURNAL   Am. J. Hum. Genet. 45 (6), 889-904 (1989)
   PUBMED   2574001
COMMENT     Original source text: Human DNA, clone lambda2D-18/2.
            Draft entry and computer-readable sequence for [Am. J. Hum. Genet.
            45, 889-904 (1989)] kindly submitted
            by S.Kimura, 29-MAR-1990.
FEATURES             Location/Qualifiers
     source          1. .9432
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="22q13.1"
     gene            join(1532. .1799,2503. .2674,3225. .3377,3466. .3626,
                     4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5909)
                     /gene="CYP2D6"
     mRNA            join(1532. .1799,2503. .2674,3225. .3377,3466. .3626,
                     4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5909)
                     /gene="CYP2D6"
                     /product="cytochrome P450 IID6"
                     /note="G00-132-127"
     exon            1532. .1799
                     /gene="CYP2D6"
                     /note="cytochrome P450 IID6; G00-132-127"
                     /number=1
     CDS             join(1620. .1799,2503. .2674,3225. .3377,3466. .3626,
                     4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5836)
                     /gene="CYP2D6"
                     /codon_start=1
                     /product="cytochrome P450 IID6"
                     /protein_id="AAA53500.1"
                     /db_xref="GI:181304"
                     /db_xref="GDB:G00-132-127"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYPPGPLPLPGLG
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                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                     MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVSPSPYELCAVPR"
     intron          1800. .2502
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=1
     exon            2503. .2674
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=2
     intron          2675. .3224
                     /gene="CYP2D6"
                     /note="G00-132-127; does not fit consensus"
                     /number=2
     exon            3225. .3377
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=3
     intron          3378. .3465
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=3
     exon            3466. .3626
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                     /note="G00-132-127"
                     /number=4
     intron          3627. .4059
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=4
     exon            4060. .4236
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=5
     intron          4237. .4426
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=5
     exon            4427. .4568
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=6
     intron          4569. .4775
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=6
     exon            4776. .4963
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                     /number=7
     intron          4964. .5417
                     /gene="CYP2D6"
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                     /note="G00-132-127"
                     /number=7
     exon            5418. .5559
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=8
     intron          5560. .5657
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=8
     exon            5658. .5909
                     /gene="CYP2D6"
                     /note="G00-132-127"
                     /number=9
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 52
AX687028
LOCUS       AX687028                9433 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2 from Patent EP1281755.
ACCESSION   AX687028
VERSION     AX687028.1  GI:29409532
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Milos,P.M. and Webb,S.M.
  TITLE     Variants of the human cyp2d6 gene
  JOURNAL   Patent: EP 1281755-A 2 05-FEB-2003;
            Pfizer Products Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9433
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 2;  Length 9433;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 53
HSCYP2D7A
LOCUS       HSCYP2D7A              13278 bp    DNA     linear   PRI 21-OCT-1992
DEFINITION  Human CYP2D7AP pseudogene for cytochrome P450 2D6.
ACCESSION   X58467
VERSION     X58467.1  GI:30336
KEYWORDS    CYP2D7AP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heim,M.H. and Meyer,U.A.
  TITLE     Evolution of a highly polymorphic human cytochrome P450 gene
            cluster: CYP2D6
  JOURNAL   Genomics 14 (1), 49-58 (1992)
  PUBMED    1358797
REFERENCE   2  (bases 1 to 13278)
  AUTHORS   Heim,M.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre
            University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND
COMMENT     See X58468, and Am. J. Hum. Genet. 47:994-1001(1990).
FEATURES             Location/Qualifiers
     source          1. .13278
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /clone="42"
                     /clone_lib="EMBL4"
                     /dev_stage="adult"
     gene            1154. .5489
                     /gene="CYP2D7AP"
                     /pseudo
     mRNA            join(1154. .1424,2125. .2296,2823. .2975,3064. .3225,
                     3651. .3827,4020. .4161,4356. .4542,4998. .5139,5238. .5489)
                     /gene="CYP2D7AP"
                     /pseudo
     exon            1154. .1424
                     /gene="CYP2D7AP"
                     /number=1
                     /pseudo
     CDS             join(1242. .1424,2125. .2296,2823. .2975,3064. .3225,
                     3651. .3827,4020. .4161,4356. .4542,4998. .5139,5238. .5416)
                     /gene="CYP2D7AP"
                     /pseudo
                     /codon_start=1
     intron          1425. .2124
                     /gene="CYP2D7AP"
                     /number=1
                     /pseudo
     exon            2125. .2296
                     /gene="CYP2D7AP"
                     /number=2
                     /pseudo
     intron          2297. .2822
                     /gene="CYP2D7AP"
                     /number=2
                     /pseudo
     exon            2823. .2975
                     /gene="CYP2D7AP"
                     /number=3
                     /pseudo
     intron          2976. .3063
                     /gene="CYP2D7AP"
                     /number=3
                     /pseudo
     exon            3064. .3225
                     /gene="CYP2D7AP"
                     /number=4
                     /pseudo
     intron          3226. .3650
                     /gene="CYP2D7AP"
                     /number=4
                     /pseudo
     exon            3651. .3827
                     /gene="CYP2D7AP"
                     /number=5
                     /pseudo
     intron          3828. .4019
                     /gene="CYP2D7AP"
                     /number=5
                     /pseudo
     exon            4020. .4161
                     /gene="CYP2D7AP"
                     /number=6
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                /pseudo
     intron     4162. .4355
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                /number=6
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     exon       4356. .4542
                /gene="CYP2D7AP"
                /number=7
                /pseudo
     intron     4543. .4997
                /gene="CYP2D7AP"
                /number=7
                /pseudo
     exon       4998. .5139
                /gene="CYP2D7AP"
                /number=8
                /pseudo
     intron     5140. .5237
                /gene="CYP2D7AP"
                /number=8
                /pseudo
     exon       5238. .5489
                /gene="CYP2D7AP"
                /number=9
                /pseudo
     repeat_region 7887. .7908
                /note="ACCCTTCCCC repeat"
ORIGIN

  Query Match           100.0%;  Score 17;  DB 5;  Length 13278;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3046 CGCATCTCCCACCCCCA 3062


RESULT 54
DQ211355
LOCUS       DQ211355               13607 bp    DNA     linear   PRI 21-OCT-2005
DEFINITION  Homo sapiens cytochrome P450 2D7 (CYP2D7P) pseudogene, partial
            sequence; and cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*36 allele,
            partial cds.
ACCESSION   DQ211355
VERSION     DQ211355.1  GI:77732539
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 13607)
  AUTHORS   Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K.,
            Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
  TITLE     Sequence-based analysis of the CYP2D6*36-CYP2D6*10 tandem-type
            arrangement, a major CYP2D6*10-harboring haplotype in the Japanese
            population
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 13607)
  AUTHORS   Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K.,
            Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-2005) Team for Pharmacogenetics, National
            Institute of Health Sciences, 1-18-1, Kamiyoga, Setagaya-ku, Tokyo
            158-8501, Japan
FEATURES             Location/Qualifiers
     source          1. .13607
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /map="22q13.31"
     gene            <429. .3022
                     /gene="CYP2D7P"
                     /pseudo
     CDS             join(<429. .581,670. .831,1257. .1433,1626. .1767,1962. .2149,
                     2604. .2745,2844. .3022)
                     /gene="CYP2D7P"
                     /note="cytochrome P450 2D7"
                     /pseudo
                     /codon_start=3
     gene            <12513. .>13566
                     /gene="CYP2D6"
                     /allele="CYP2D6*36"
     mRNA            join(<12513. .12692,13395. .>13566)
                     /gene="CYP2D6"
                     /allele="CYP2D6*36"
                     /product="cytochrome P450 2D6"
     CDS             join(12513. .12692,13395. .>13566)
                     /gene="CYP2D6"
                     /allele="CYP2D6*36"
                     /EC_number="1.14.14.1"
                     /note="debrisoquine 4-hydroxylase"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB01373.1"
                     /db_xref="GI:77732540"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYSPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQ"
ORIGIN

  Query Match           100.0%;  Score 17;  DB 5;  Length 13607;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        652 CGCATCTCCCACCCCCA 668


RESULT 55
HSCYP2D7B
LOCUS       HSCYP2D7B              13677 bp    DNA     linear   PRI 21-OCT-1992
DEFINITION  Human CYP2D7BP pseudogene for cytochrome P450 2D6.
ACCESSION   X58468
VERSION     X58468.1  GI:30337
KEYWORDS    CYP2D7BP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heim,M.H. and Meyer,U.A.
  TITLE     Evolution of a highly polymorphic human cytochrome P450 gene
            cluster: CYP2D6
  JOURNAL   Genomics 14 (1), 49-58 (1992)
  PUBMED    1358797
REFERENCE   2  (bases 1 to 13677)
  AUTHORS   Heim,M.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre
            University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND
COMMENT     See X58467, and Am. J. Hum. Genet. 47:994-1001(1990).
FEATURES             Location/Qualifiers
     source          1. .13677
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /clone="45"
                     /clone_lib="EMBL4"
                     /dev_stage="adult"
     gene            1534. .5868
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                /gene="CYP2D7BP"
                /pseudo
     mRNA       join(1534. .1801,2504. .2675,3203. .3355,3444. .3605,
                4031. .4207,4400. .4540,4735. .4922,5377. .5518,5617. .5868)
                /gene="CYP2D7BP"
                /pseudo
     exon       1534. .1801
                /gene="CYP2D7BP"
                /number=1
                /pseudo
     CDS        join(1622. .1801,2504. .2675,3203. .3355,3444. .3605,
                4031. .4207,4400. .4540,4735. .4922,5377. .5518,5617. .5795)
                /gene="CYP2D7BP"
                /pseudo
                /codon_start=1
     intron     1802. .2503
                /gene="CYP2D7BP"
                /number=1
                /pseudo
     exon       2504. .2675
                /gene="CYP2D7BP"
                /number=2
                /pseudo
     intron     2676. .3202
                /gene="CYP2D7BP"
                /number=2
                /pseudo
     exon       3203. .3355
                /gene="CYP2D7BP"
                /number=3
                /pseudo
     intron     3356. .3443
                /gene="CYP2D7BP"
                /number=3
                /pseudo
     exon       3444. .3605
                /gene="CYP2D7BP"
                /number=4
                /pseudo
     intron     3606. .4030
                /gene="CYP2D7BP"
                /number=4
                /pseudo
     exon       4031. .4207
                /gene="CYP2D7BP"
                /number=5
                /pseudo
     intron     4208. .4399
                /gene="CYP2D7BP"
                /number=5
                /pseudo
     exon       4400. .4540
                /gene="CYP2D7BP"
                /number=6
                /pseudo
     intron     4541. .4734
                /gene="CYP2D7BP"
                /number=6
                /pseudo
     exon       4735. .4922
                /gene="CYP2D7BP"
                /number=7
                /pseudo
     intron     4923. .5376
                /gene="CYP2D7BP"
                /number=7
                /pseudo
     exon       5377. .5518
                /gene="CYP2D7BP"
                /number=8
                /pseudo
     intron     5519. .5616
                /gene="CYP2D7BP"
                /number=8
                /pseudo
     exon       5617. .5868
                /gene="CYP2D7BP"
                /number=9
                /pseudo
     repeat_region 8267. .8306
                /note="ACCCTTCCCC"
ORIGIN

  Query Match            100.0%;  Score 17;  DB 5;  Length 13677;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3426 CGCATCTCCCACCCCCA 3442


RESULT 56
HUMCYP8P
LOCUS       HUMCYP8P               17060 bp    DNA     linear   PRI 09-NOV-1994
DEFINITION  Human debrisoquine 4-hydroxylase (CYP2D8P) and (CYP2D7) pseudogenes
            complete sequences.
ACCESSION   M33387
VERSION     M33387.1  GI:181320
KEYWORDS    debrisoquine 4-hydroxylase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 17060)
  AUTHORS   Kimura,S., Umeno,M., Skoda,R.C., Meyer,U.A. and Gonzalez,F.J.
  TITLE     The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and
            identification of the polymorphic CYP2D6 gene, a related gene, and
            a pseudogene
  JOURNAL   Am. J. Hum. Genet. 45 (6), 889-904 (1989)
   PUBMED   2574001
COMMENT     Original source text: Human DNA, clones lambda-2D-A and
            lambda-2D-B.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by S.Kimura, 29-MAR-1990.
FEATURES             Location/Qualifiers
     source          1. .17060
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     TATA_signal     1276. .1282
     prim_transcript 1304. .6570
                     /note="CYP2D8P mRNA and introns"
     gene            join(1392. .1568,3189. .3360,3907. .4059,4148. .4310,
                     4758. .4934,5121. .5262,5467. .5651,6101. .6242,6339. .6516)
                     /gene="CYP2D8P"
     CDS             join(1392. .1568,3189. .3360,3907. .4059,4148. .4310,
                     4758. .4934,5121. .5262,5467. .5651,6101. .6242,6339. .6516)
                     /gene="CYP2D8P"
                     /pseudo
                     /codon_start=1
                     /product="debrisoquine 4-hydroxylase"
     exon            <1392. .1568
                     /gene="CYP2D8P"
                     /number=1
     exon            3189. .3360
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                     /number=2
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     exon            3907. .4059
                     /gene="CYP2D8P"
                     /number=3
                     /pseudo
     exon            4148. .4310
                     /gene="CYP2D8P"
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                     /number=4
                     /pseudo
     exon            4758. .4934
                     /gene="CYP2D8P"
                     /number=5
                     /pseudo
     exon            5121. .5262
                     /gene="CYP2D8P"
                     /number=6
                     /pseudo
     exon            5467. .5651
                     /gene="CYP2D8P"
                     /number=7
                     /pseudo
     exon            6101. .6242
                     /gene="CYP2D8P"
                     /number=8
                     /pseudo
     exon            6339. .>6516
                     /gene="CYP2D8P"
                     /number=9
     TATA_signal     11209. .11215
     prim_transcript 11236. .15571
                     /note="CYP2D7 mRNA and introns"
     gene            join(11324. .11504,12206. .12377,12906. .13058,13147. .13307,
                     13733. .13909,14102. .14243,14438. .14625,15080. .15221,
                     15320. .15496)
                     /gene="CYP2D7"
     CDS             join(11324. .11504,12206. .12377,12906. .13058,13147. .13307,
                     13733. .13909,14102. .14243,14438. .14625,15080. .15221,
                     15320. .15496)
                     /gene="CYP2D7"
                     /pseudo
                     /codon_start=1
                     /product="debrisoquine 4-hydroxylase"
     exon            <11324. .11504
                     /gene="CYP2D7"
                     /number=1
     exon            12206. .12377
                     /gene="CYP2D7"
                     /number=2
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     exon            12906. .13058
                     /gene="CYP2D7"
                     /number=3
                     /pseudo
     exon            13147. .13307
                     /gene="CYP2D7"
                     /number=4
                     /pseudo
     exon            13733. .13909
                     /gene="CYP2D7"
                     /number=5
                     /pseudo
     exon            14102. .14243
                     /gene="CYP2D7"
                     /number=6
                     /pseudo
     exon            14438. .14625
                     /gene="CYP2D7"
                     /number=7
                     /pseudo
     exon            15080. .15221
                     /gene="CYP2D7"
                     /number=8
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     exon            15320. .>15496
                     /gene="CYP2D7"
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ORIGIN

  Query Match           100.0%;  Score 17;  DB 5;  Length 17060;
  Best Local Similarity 100.0%;  Pred. No. 1.3e+03;

  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db      13129 CGCATCTCCCACCCCCA 13145


RESULT 57
DQ211354
LOCUS       DQ211354               20337 bp    DNA     linear   PRI 21-OCT-2005
DEFINITION  Homo sapiens cytochrome P450 2D7 (CYP2D7P) pseudogene, partial
            sequence; and cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*10 allele,
            complete cds.
ACCESSION   DQ211354
VERSION     DQ211354.1  GI:77732537
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 20337)
  AUTHORS   Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K.,
            Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
  TITLE     Sequence-based analysis of the CYP2D6*36-CYP2D6*10 tandem-type
            arrangement, a major CYP2D6*10-harboring haplotype in the Japanese
            population
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 20337)
  AUTHORS   Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K.,
            Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-2005) Team for Pharmacogenetics, National
            Institute of Health Sciences, 1-18-1, Kamiyoga, Setagaya-ku, Tokyo
            158-8501, Japan
FEATURES             Location/Qualifiers
     source          1. .20337
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <429. .3022
                     /gene="CYP2D7P"
                     /pseudo
     CDS             join(<429. .581,670. .831,1257. .1433,1626. .1767,1962. .2149,
                     2604. .2745,2844. .3022)
                     /gene="CYP2D7P"
                     /note="cytochrome P450 2D7"
                     /pseudo
                     /codon_start=3
     gene            <12513. .>16730
                     /gene="CYP2D6"
                     /allele="CYP2D6*10"
     mRNA            join(<12513. .12692,13395. .13566,14119. .14271,14360. .14520,
                     14954. .15130,15321. .15462,15670. .15857,16312. .16453,
                     16552. .>16730)
                     /gene="CYP2D6"
                     /allele="CYP2D6*10"
                     /product="cytochrome P450 2D6"
     CDS             join(12513. .12692,13395. .13566,14119. .14271,14360. .14520,
                     14954. .15130,15321. .15462,15670. .15857,16312. .16453,
                     16552. .16730)
                     /gene="CYP2D6"
                     /allele="CYP2D6*10"
                     /EC_number="1.14.14.1"
                     /note="debrisoquine 4-hydroxylase"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB01372.1"
                     /db_xref="GI:77732538"
                     /translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYSPGPLPLPGLG
                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
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FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"

ORIGIN

Query Match 100.0%; Score 17; DB 5; Length 20337;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 652 CGCATCTCCCACCCCCA 668

RESULT 58
DQ211353
LOCUS DQ211353 23381 bp DNA linear PRI 19-OCT-2005
DEFINITION Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*36 allele and cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*10 allele, complete cds.
ACCESSION DQ211353
VERSION DQ211353.1 GI:77732534
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 23381)
AUTHORS Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K., Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
TITLE Sequence-based analysis of the CYP2D6*36-CYP2D6*10 tandem-type arrangement, a major CYP2D6*10-harboring haplotype in the Japanese population
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 23381)
AUTHORS Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K., Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-2005) Team for Pharmacogenetics, National Institute of Health Sciences, 1-18-1, Kamiyoga, Setagaya-ku, Tokyo 158-8501, Japan
FEATURES Location/Qualifiers
source 1. .23381
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="22"
/map="22q13.31"
gene <1849. .>6066
/gene="CYP2D6"
/allele="CYP2D6*36"
mRNA join(<1849. .2028,2731. .2902,3455. .3607,3696. .3856, 4290. .4466,4657. .4798,5006. .5193,5648. .5789,5888. .>6066)
/gene="CYP2D6"
/allele="CYP2D6*36"
/product="cytochrome P450 2D6"
CDS join(1849. .2028,2731. .2902,3455. .3607,3696. .3856, 4290. .4466,4657. .4798,5006. .5193,5648. .5789,5888. .6066)
/gene="CYP2D6"
/allele="CYP2D6*36"
/EC_number="1.14.14.1"
/note="debrisoquine 4-hydroxylase"
/codon_start=1
/product="cytochrome P450 2D6"
/protein_id="ABB01370.1"
/db_xref="GI:77732535"
/translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYSPGPLPLPGLG
NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
gene <15557. .>19774
/gene="CYP2D6"
/allele="CYP2D6*10"
mRNA join(<15557. .15736,16439. .16610,17163. .17315,17404. .17564, 17998. .18174,18365. .18506,18714. .18901,19356. .19497, 19596. .>19774)
/gene="CYP2D6"
/allele="CYP2D6*10"
/product="cytochrome P450 2D6"
CDS join(15557. .15736,16439. .16610,17163. .17315,17404. .17564, 17998. .18174,18365. .18506,18714. .18901,19356. .19497, 19596. .19774)
/gene="CYP2D6"
/allele="CYP2D6*10"
/EC_number="1.14.14.1"
/note="debrisoquine 4-hydroxylase"
/codon_start=1
/product="cytochrome P450 2D6"
/protein_id="ABB01371.1"
/db_xref="GI:77732536"
/translation="MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYSPGPLPLPGLG
NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"

ORIGIN

Query Match 100.0%; Score 17; DB 5; Length 23381;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
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Db 3678 CGCATCTCCCACCCCCA 3694

RESULT 59
HS257I20/c
LOCUS HS257I20 114846 bp DNA linear PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone RP1-257I20 on chromosome 22q13.1-13.2 Contains the 3' end of a novel gene, CYP2D7AP and CYP2D8P (cytochrome P450) pseudogenes,part of the TCF20 gene for transcription factor 20 (AR1, KIAA0292), the NDUFA6 gene for NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 6, a pseudogene similar to GTP-binding protein genes, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.
ACCESSION AL021878
VERSION AL021878.2 GI:17065905
KEYWORDS HTG; AR1; ca repeat polymorphism; CYP2D7AP; CYP2D8P; cytochrome; KIAA0292; NADH dehydrogenase; NDUFA6; TCF20.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 114846)
AUTHORS Bridgeman,A.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Nov 25, 2001 this sequence version replaced gi:3204432.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

```
          Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
          on the WORMPEP database can be found at
          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
          was generated from part of bacterial clone contigs of human
          chromosome 22, constructed by the Sanger Centre Chromosome 22
          Mapping Group.  Further information can be found at
          http://www.sanger.ac.uk/HGP/Chr22
          RP1-257I20 is from the library RPCI-1 constructed by the group of
          Pieter de Jong. For further details see
          http://www.chori.org/bacpac/home.htm
          VECTOR: pCYPAC2
          -------------- Genome Center
          Center: Wellcome Trust Sanger Institute
          Center code: SC
          Web site: http://www.sanger.ac.uk
          Contact: vega@sanger.ac.uk
          --------------
          This sequence was finished as follows unless otherwise noted: all
          regions were either double-stranded or sequenced with an alternate
          chemistry or covered by high quality data (i.e., phred quality >=
          30); an attempt was made to resolve all sequencing problems, such
          as compressions and repeats; all regions were covered by at least
          one subclone; and the assembly was confirmed by restriction digest,
          except on the rare occasion of the clone being a YAC.
FEATURES             Location/Qualifiers
     source          1. .114846
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="RZPD:RPCIP704I20257"
                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /map="q13.1-13.2"
                     /clone="RP1-257I20"
                     /clone_lib="RPCI-1"
     misc_feature    1
                     /note="Clone_left_end: RP1-257I20"
     gene            join(Z82192.1:2136. .2399,Z82192.1:4370. .4504,101. .106,
                     1160. .1402)
                     /locus_tag="RP1-257I20.4-001"
     mRNA            join(Z82192.1:2136. .2399,Z82192.1:4370. .4504,101. .106,
                     1160. .1402)
                     /locus_tag="RP1-257I20.4-001"
     gene            join(Z82192.1:4405. .4504,101. .106,1160. .1394)
                     /locus_tag="RP1-257I20.9-001"
     mRNA            join(Z82192.1:4405. .4504,101. .106,1160. .1394)
                     /locus_tag="RP1-257I20.9-001"
     CDS             join(Z82192.1:2214. .2399,Z82192.1:4370. .4504,101. .103)
                     /locus_tag="RP1-257I20.9-001"
                     /standard_name="OTTHUMP00000028567"
                     /codon_start=1
                     /protein_id="CAI19952.1"
                     /db_xref="GI:56202716"
                     /db_xref="UniProtKB/TrEMBL:Q9H4I9"
                     /translation="MASGAARWLVLAPVRSGALRSGPSLRKDGDVSAAWSGSGRSLVP
                     SRSVIVTRSGAILPKPVKMSFGLLRVFSIVIPFLYVGTLISKNFAALLEEHDIFVPED
                     DDDDD"
     gene            complement(3567. .9000)
                     /locus_tag="RP1-257I20.3-001"
     mRNA            complement(join(3567. .4355,5101. .5216,8647. .9000))
                     /locus_tag="RP1-257I20.3-001"
                     /note="match: cDNAs: Em:AF047182.1 Em:BC002772.1
                     Em:CR456529.1 Em:CR620155.1"
     CDS             complement(join(4224. .4355,5101. .5216,8647. .8863))
                     /locus_tag="RP1-257I20.3-001"
                     /standard_name="OTTHUMP00000028595"
                     /note="match: proteins: Q6IBT8 Q6IC39 Sw:P56556 Sw:Q02366"
                     /codon_start=1
                     /protein_id="CAI19953.1"
                     /db_xref="GI:56202717"
                     /db_xref="GOA:P56556"
                     /db_xref="UniProtKB/Swiss-Prot:P56556"
                     /translation="MGKDIRPRSARAACKGVGLWSGCFGKMAGSGVRQATSTASTFVK
                     PIFSRDMNEAKRRVRELYRAWYREVPNTVHQFQLDITVKMGRDKVREMFMKNAHVTDP
                     RVVDLLVIKGKIELEETIKVWKQRTHVMRFFHETEAPRPKDFLSKFYVGHDP"
     misc_feature    20171
                     /note="Clone_right_end: RP1-186O1"
     gene            complement(25824. .26994)
                     /locus_tag="RP1-257I20.10-001"
                     /pseudo
     CDS             complement(25824. .26994)
                     /locus_tag="RP1-257I20.10-001"
                     /pseudo
                     /codon_start=1
     polyA_site      complement(46092)
     polyA_signal    complement(46110. .46115)
     misc_feature    99274. .99444
                     /note="Other . Weak data"
     misc_feature    114846
                     /note="Clone_right_end: RP1-257I20"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 5;  Length 114846;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db      48546 CGCATCTCCCACCCCCA 48530


RESULT 60
BX247885/c
LOCUS       BX247885              133246 bp    DNA     linear   PRI 18-MAY-2005
DEFINITION  Human DNA sequence from clone RP4-669P10 on chromosome
            22q13.31-13.33, complete sequence.
ACCESSION   BX247885
VERSION     BX247885.11  GI:30524848
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 133246)
  AUTHORS   Lloyd,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On May 10, 2003 this sequence version replaced gi:30230961.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 22, constructed by the Sanger Centre Chromosome 22
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr22
            RP4-669P10 is from the library RPCI-4 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pCYPAC2
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one subclone; and the assembly was confirmed by restriction digest,
            except on the rare occasion of the clone being a YAC.
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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /map="q13.31-13.33"
                     /clone="RP4-669P10"
                     /clone_lib="RPCI-4"
     misc_feature    1
                     /note="Clone_left_end: RP4-669P10"
     gene            join(3534. .3617,4007. .4049,4362. .4513)
                     /locus_tag="RP4-669P10.8-006"
     mRNA            join(3534. .3617,4007. .4049,4362. .4513)
                     /locus_tag="RP4-669P10.8-006"
     gene            join(5457. .6236,7326. .7467,7658. .7834,8268. .8428,
                     20048. .20189,20644. .20831,22211. .22363,22727. .22839,
                     22883. .23087,23767. .23947)
                     /locus_tag="RP4-669P10.1-001"
                     /pseudo
     CDS             join(5457. .6236,7326. .7467,7658. .7834,8268. .8428,
                     20048. .20189,20644. .20831,22211. .22363,22727. .22839,
                     22883. .23087,23767. .23947)
                     /locus_tag="RP4-669P10.1-001"
                     /pseudo
                     /codon_start=1
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                     /note="Single clone region. Sequence generated from a
                     transposon library derived from a single pUC clone.
                     Restriction digest data confirm the assembly."
                     /pseudo
     gene            complement(join(29359. .29537,29636. .29777,30228. .30412,
                     30617. .30758,30945. .31121,31569. .31731,31820. .31972,
                     32521. .32692,34313. .34489))
                     /locus_tag="RP4-669P10.5-001"
                     /pseudo
     CDS             complement(join(29359. .29537,29636. .29777,30228. .30412,
                     30617. .30758,30945. .31121,31569. .31731,31820. .31972,
                     32521. .32692,34313. .34489))
                     /locus_tag="RP4-669P10.5-001"
                     /pseudo
                     /codon_start=1
     gene            complement(join(39501. .40846,48097. .48224,49335. .49384,
                     59097. .59190,89139. .94930))
                     /locus_tag="RP1-257I20.2-001"
     mRNA            complement(join(39501. .40846,48097. .48224,49335. .49384,
                     59097. .59190,89139. .94930))
                     /locus_tag="RP1-257I20.2-001"
     gene            complement(join(<39564. .40846,48097. .48224,49335. .49384,
                     59097. .>59190))
                     /gene="TCF20"
                     /locus_tag="RP4-669P10.13-002"
     mRNA            complement(join(<39564. .40846,48097. .48224,49335. .49384,
                     59097. .>59190))
                     /gene="TCF20"
                     /locus_tag="RP4-669P10.13-002"
                     /note="match: ESTs: AA414032 AA877828 AI220580 AI693830.1
                     AU017455
                     match: cDNAs: AB006630 U19345 U20282"
     gene            complement(join(<40602. .40846,49331. .49384,59097. .>59190))
                     /gene="TCF20"
                     /locus_tag="RP4-669P10.13-001"
     mRNA            complement(join(<40602. .40846,49331. .49384,59097. .>59190))
                     /gene="TCF20"
                     /locus_tag="RP4-669P10.13-001"
                     /note="match: ESTs: AA414032 AA877828 AI220580 AI693830.1
                     AU017455 H55457 H55458
                     match: cDNAs: U19345 U20282"
     CDS             complement(join(<40602. .40846,49331. .49384,59097. .>59190))
                     /gene="TCF20"
                     /locus_tag="RP4-669P10.13-001"
                     /standard_name="OTTHUMP00000042203"
                     /note="match: proteins: O14686 O93321 Q13078"
                     /codon_start=1
                     /protein_id="CAI43005.1"
                     /db_xref="GI:57209875"
                     /db_xref="GOA:Q5HYV9"
                     /db_xref="UniProtKB/TrEMBL:Q5HYV9"
                     /translation="KCSHCQEAGATLGCYNKGCSFRYHYPCAIDADCLLHEENFSVRC
                     PKHKVSETVEMRRWWTLVMEWKSSYRAATPCPAPPRPARVPAHASTSLSSHITLKPVT
                     PQERKTQDVGMAVSMDTISIVTMWGEGGG"
     CDS             complement(join(48141. .48224,49335. .49384,59097. .59190,
                     89139. .94793))
                     /locus_tag="RP1-257I20.2-001"
                     /standard_name="OTTHUMP00000028889"
                     /codon_start=1
                     /protein_id="CAI95721.1"
                     /db_xref="GI:66347846"
                     /translation="MQSFREQSSYHGNQQSYPQEVHGSSRLEEFSPRQAQMFQNFGGT
                     GGSSGSSGSGSGGGRRGAAAAAAAMASETSGHQGYQGFRKEAGDFYYMAGNKDPVTTG
                     TPQPPQRRPSGPVQSYGPPQGSSFGNQYGSEGHVGQFQAQHSGLGGVSHYQQDYTGPF
                     SPGSAQYQQQASSQQQQQQVQQLRQQLYQSHQPLPQATGQPASSSSHLQPMQRPSTLP
                     SSAAGYQLRVGQFGQHYQSSASSSSSSSFPSPQRFSQSGQSYDGSYNVNAGSQYEGHN
                     VGSNAQAYGTQSNYSYQPQSMKNFEQAKIPQGTQQGQQQQQPQQQQHPSQHVMQYTNA
                     ATKLPLQSQVGQYNQPEVPVRSPMQFHQNFSPISNPSPAASVVQSPSCSSTPSPLMQT
                     GENLQCGQGSVPMGSRNRILQLMPQLSPTPSMMPSPNSHAAGFKGFGLEGVPEKRLTD
                     PGLSSLSALSTQVANLPNTVQHMLLSDALTPQKKTSKRPSSSKKADSCTNSEGSSQPE
                     EQLKSPMAESLDGGCSSSSEDQGERVRQLSGQSTSSDTTYKGGASEKAGSSPAQGAQN
                     EPPRLNASPAAREEATSPGAKDMPLSSDGNPKVNEKTVGVIVSREAMTGRVEKPGGQD
                     KGSQEDDPAATQRPPSNGGAKETSHASLPQPEPPGGGGSKGNKNGDNNSNHNGEGNGQ
                     SGHSAAGPGFTSRTEPSKSPGSLRYSYKDSFGSAVPRNVSGFPQYPTGQEKGDFTGHG
                     ERKGRNEKFPSLLQEVLQGYHHHPDRRYSRSTQEHQGMAGSLEGTTRPNVLVSQTNEL
                     ASRGLLNKSIGSLLENPHWGPWERKSSSTAPEMKQINLTDYPIPRKFEIEPQSSAHEP
                     GGSLSERRSVICDISPLRQIVRDPGAHSLGHMSADTRIGRNDRLNPTLSQSVILPGGL
                     VSMETKLKSQSGQIKEEDFEQSKSQASFNNKKSGDHCHPPSIKHESYRGNASPGAATH
                     DSLSDYGPQDSRPTPMRRVPGRVGGREGMRGRSPSQYHDFAEKLKMSPGRSRGPGGDP
                     HHMNPHMTFSERANRSSLHTPFSPNSETLASAYHANTRAHAYGDPNAGLNSQLHYKRQ
                     MYQQQPEEYKDWSSGSAQGVIAAAQHRQEGPRKSPRQQQFLDRVRSPLKNDKDGMMYG
                     PPVGTYHDPSAQEAGRCLMSSDGLPNKGMELKHGSQKLQESCWDLSRQTSPAKSSGPP
                     GMSSQKRYGPPHETDGHGLAEATQSSKPGSVMLRLPGQEDHSSQNPLIMRRRVRSFIS
                     PIPSKRQSQDVKNSSTEDKGRLLHSSKEGADKAFNSYAHLSHSQDIKSIPKRDSSKDL
                     PSPDSRNCPAVTLTSPAKTKILPPRKGRGLKLEAIVQKITSPNIRRSASSNSAEAGGD
                     TVTLDDILSLKSGPPEGGSVAVQDADIEKRKGEVASDLVSPANQELHVEKPLPRSSEE
                     WRGSVDDKVKTETHAETVTAGKEPPGAMTSTTSQKPGSNQGRPDGSLGGTAPLIFPDS
                     KNVPPVGILAPEANPKAEEKENDTVTISPKQEGFPPKGYFPSGKKKGRPIGSVNKQKK
                     QQQPPPPPPQPPQIPEGSADGEPKPKKQRQRRERRKPGAQPRKRKTKQAVPIVEPQEP
                     EIKLKYATQPLDKTDAKNKSFYPYIHVVNKCELGAVCTIINAEEEEQTKLVRGRKGQR
                     SLTPPPSSTESKALPASSFMLQGPVVTESSVMGHLVCCLCGKWASYRNMGDLFGPFYP
                     QDYAATLPKNPPPKRATEMQSKVKVRHKSASNGSKTDTEEEEEQQQQQKEQRSLAAHP
                     RFKRRHRSEDCGGGPRSLSRGLPCKKAATEGSSEKTVLDSKPSVPTTSEGGPELELQI
                     PELPLDSNEFWVHEGCILWANGIYLVCGRLYGLQEALEIAREMKCSHCQEAGATLGCY
                     NKGCSFRYHYPCAIDADCLLHEENFSVRCPKHKPPLPCPLPPLQNKTAKGSLSTEQSE
                     RG"
     CDS             complement(join(48141. .48224,49335. .49384,59097. .>59190))
                     /gene="TCF20"
                     /locus_tag="RP4-669P10.13-002"
                     /standard_name="OTTHUMP00000042204"
                     /note="match: proteins: O14528"
                     /codon_start=1
                     /protein_id="CAI43006.1"
                     /db_xref="GI:57209876"
                     /db_xref="GOA:Q5HYV8"
                     /db_xref="UniProtKB/TrEMBL:Q5HYV8"
                     /translation="KCSHCQEAGATLGCYNKGCSFRYHYPCAIDADCLLHEENFSVRC
                     PKHKPPLPCPLPPLQNKTAKGSLSTEQSERG"
     misc_feature    133246
                     /note="Clone_right_end: RP4-669P10"
ORIGIN

  Query Match          100.0%;  Score 17;  DB 5;  Length 133246;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
```

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Db      22140 CGCATCTCCCACCCCCA 22124


RESULT 61
BX855600
LOCUS       BX855600              176354 bp    DNA     linear   HTG 06-DEC-2003
DEFINITION  Mus musculus chromosome 2 clone RP24-329I19, *** SEQUENCING IN
            PROGRESS ***, 17 unordered pieces.
ACCESSION   BX855600
VERSION     BX855600.1  GI:39540463
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 176354)
  AUTHORS   Sims,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-DEC-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     Sequence from the Mouse Genome Sequencing Consortium whole genome
            shotgun may have been used to confirm this sequence.  Sequence data
            from the whole genome shotgun alone has only been used where it has
            a phred quality of at least 30.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bN329I19
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: Dye-terminator; 100% of reads
            Consensus quality: 171626 bases at least Q40
            Consensus quality: 172662 bases at least Q30
            Consensus quality: 173439 bases at least Q20
            Insert size: 174754; sum-of-contigs
            Insert size: 193637; 2.5% error; agarose-fp
            Quality coverage: 6.07x in Q20 bases; sum-of-contigs Quality
            coverage: 5.72x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 17 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    12915: contig of 12915 bp in length
            *    12916    13015: gap of 100 bp
            *    13016    17657: contig of 4642 bp in length
            *    17658    17757: gap of 100 bp
            *    17758    24225: contig of 6468 bp in length
            *    24226    24325: gap of 100 bp
            *    24326    39950: contig of 15625 bp in length
            *    39951    40050: gap of 100 bp
            *    40051    43993: contig of 3943 bp in length
            *    43994    44093: gap of 100 bp
            *    44094    46915: contig of 2822 bp in length
            *    46916    47015: gap of 100 bp
            *    47016    52193: contig of 5178 bp in length
            *    52194    52293: gap of 100 bp
            *    52294    62884: contig of 10591 bp in length
            *    62885    62984: gap of 100 bp
            *    62985    67712: contig of 4728 bp in length
            *    67713    67812: gap of 100 bp
            *    67813    73163: contig of 5351 bp in length
            *    73164    73263: gap of 100 bp
            *    73264    78102: contig of 4839 bp in length
            *    78103    78202: gap of 100 bp
            *    78203    95806: contig of 17604 bp in length
            *    95807    95906: gap of 100 bp
            *    95907   102852: contig of 6946 bp in length
            *   102853   102952: gap of 100 bp
            *   102953   105943: contig of 2991 bp in length
            *   105944   106043: gap of 100 bp
            *   106044   130763: contig of 24720 bp in length
            *   130764   130863: gap of 100 bp
            *   130864   171000: contig of 40137 bp in length
            *   171001   171100: gap of 100 bp
            *   171101   176354: contig of 5254 bp in length.
FEATURES             Location/Qualifiers
     source          1. .176354
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="2"
                     /clone="RP24-329I19"
                     /clone_lib="RPCI-24"
     misc_feature    1. .12915
                     /note="assembly_fragment:00729
                     fragment_chain:1
                     clone_end:SP6
                     vector_side:left"
     misc_feature    13016. .17657
                     /note="assembly_fragment:00214
                     fragment_chain:1"
     misc_feature    17758. .24225
                     /note="assembly_fragment:00532
                     fragment_chain:1"
     misc_feature    24326. .39950
                     /note="assembly_fragment:00877
                     fragment_chain:2"
     misc_feature    40051. .43993
                     /note="assembly_fragment:00140
                     fragment_chain:2"
     misc_feature    44094. .46915
                     /note="assembly_fragment:00086
                     fragment_chain:2"
     misc_feature    47016. .52193
                     /note="assembly_fragment:00300
                     fragment_chain:2"
     misc_feature    52294. .62884
                     /note="assembly_fragment:00603
                     fragment_chain:2"
     misc_feature    62985. .67712
                     /note="assembly_fragment:00176
                     fragment_chain:2"
     misc_feature    67813. .73163
                     /note="assembly_fragment:00345
                     fragment_chain:2"
     misc_feature    73264. .78102
                     /note="assembly_fragment:00257
                     fragment_chain:2"
     misc_feature    78203. .95806
                     /note="assembly_fragment:01044
                     fragment_chain:2"
     misc_feature    95907. .102852
                     /note="assembly_fragment:00395
                     fragment_chain:3"
     misc_feature    102953. .105943
                     /note="assembly_fragment:00110
                     fragment_chain:3"
     misc_feature    106044. .130763
                     /note="assembly_fragment:01224
                     fragment_chain:4"
     misc_feature    130864. .171000
                     /note="assembly_fragment:01491
                     fragment_chain:4"
     misc_feature    171101. .176354
                     /note="assembly_fragment:00462"
ORIGIN
```

```
  Query Match             100.0%;  Score 17;  DB 12;  Length 176354;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db     171933 CGCATCTCCCACCCCCA 171949


RESULT 62
AL805970/c
LOCUS       AL805970              180421 bp    DNA     linear   ROD 15-SEP-2002
DEFINITION  Mouse DNA sequence from clone RP23-438O3 on chromosome 4, complete
            sequence.
ACCESSION   AL805970
VERSION     AL805970.8  GI:23093706
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 180421)
  AUTHORS   Phillimore,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Sep 17, 2002 this sequence version replaced gi:22798304.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            --------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-438O3 is
            from the RPCI-23 Mouse PAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .180421
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="4"
                     /clone="RP23-438O3"
                     /clone_lib="RPCI-23"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 6;  Length 180421;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db      40413 CGCATCTCCCACCCCCA 40397


RESULT 63
AL589870
LOCUS       AL589870              202686 bp    DNA     linear   ROD 05-APR-2002
DEFINITION  Mouse DNA sequence from clone RP23-118A2 on chromosome 2, complete
            sequence.
ACCESSION   AL589870
VERSION     AL589870.30  GI:20068449
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Dunn,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Apr 7, 2002 this sequence version replaced gi:17976583.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-118A2 is
            from the RPCI-23 Mouse PAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .202686
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="2"
                     /clone="RP23-118A2"
                     /clone_lib="RPCI-23"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 6;  Length 202686;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       9728 CGCATCTCCCACCCCCA 9744


RESULT 64
BX324228
LOCUS       BX324228              208652 bp    DNA     linear   HTG 24-SEP-2003
DEFINITION  Mus musculus chromosome 2 clone RP23-7A16.
ACCESSION   BX324228
VERSION     BX324228.7  GI:35209637
KEYWORDS    HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE      Mus musculus (house mouse)
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 208652)
  AUTHORS   Mashreghi-Mohammadi,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Sep 24, 2003 this sequence version replaced gi:33468655.
            Sequence from the Mouse Genome Sequencing Consortium whole genome
            shotgun may have been used to confirm this sequence.  Sequence data
            from the whole genome shotgun alone has only been used where it has
            a phred quality of at least 30.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bM7A16
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: Dye-terminator; 100% of reads
            Consensus quality: 207942 bases at least Q40
            Consensus quality: 207994 bases at least Q30
            Consensus quality: 208018 bases at least Q20
            Insert size: 208652; sum-of-contigs
            Insert size: 211673; 10.2% error; agarose-fp
            Quality coverage: 8.22x in Q20 bases; sum-of-contigs Quality
            coverage: 8.24x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1   208652: contig of 208652 bp in length.
FEATURES              Location/Qualifiers
     source           1. .208652
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:10090"
                      /chromosome="2"
                      /clone="RP23-7A16"
                      /clone_lib="RPCI-23"
     misc_feature     1. .208652
                      /note="assembly_fragment:03408"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 12;  Length 208652;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db      17836 CGCATCTCCCACCCCCA 17852


RESULT 65
AC173198/c
LOCUS       AC173198              211176 bp    DNA     linear   HTG 09-FEB-2006
DEFINITION  Bos taurus clone CH240-138G11, WORKING DRAFT SEQUENCE, 17 unordered
            pieces.
ACCESSION   AC173198
VERSION     AC173198.3  GI:87081549
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 211176)
  AUTHORS   Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,
            Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,
            Beraducci,A., Biswalo,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,
            Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I.,
            Chacko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G., Chen,R.,
            Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A.,
            Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De
            Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H.,
            Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Durbin,K.,
            Dziuda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M.,
            Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
            Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T.,
            Gaskin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D.,
            Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeberlen,K.,
            Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Havlak,P.,
            Hawes,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J.,
            Hines,S., Hitchens,M., Hodgson,A., Hogues,M., Hollins,B.,
            Howell,L.T., Hulyk,S., Hume,J., Imo,K., Jackson,A., Jackson,L.,
            Jacob,L., Jiang,H., Johnson,B., Johnson,R., Kalafus,K., Kelly,S.,
            Keys,T., Khan,Z., King,L., Kovar,C., Kowis,A., Kowis,C., Lara,F.,
            Leal,S., Lee,K., Lee,S., LeGall,F.I., Lemon,S., Lewis,L., Li,B.,
            Li,Y., Li,Z., Linnell,M., Liu,W., Liu,Y.-S., Liu,Y., Liyanage,D.,
            London,P., Lopez,J., Lorensuhewa,L., Lozado,R., Luk,T., Madu,R.,
            Maheshwari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E.,
            McClelland,H., McPherson,J., Mercadao,C., Metzker,M.,
            Milosavljevic,A., Minja,E., Morgan,M., Morris,S., Munidasa,M.,
            Murray,D., Nazarith,L., Ngo,D., Nguyen,N., Norwig-Eastaugh,E.,
            Nott,A., Nwaokelemeh,O., Obregon,M., Ochi-Okorie,C., Odeh,E.,
            Okwuonu,G., Okwuonu,K., Parker,D., Pasternak,S., Patel,B.,
            Patel,V., Paul,H., Perez,A., Perez,L., Petrosino,J., Pham,T.,
            Primus,E., Pu,L.-L., Puazo,M., Qin,X., Quinn,A., Quiroz,J.,
            Rabata,D., Rachlin,E., Reigh,R., Ren,Y., Reuter,M., Richards,S.,
            Rives,C., Rodriguez,F., Rojas,A., Ruiz,S.J., Sana,M., Sanders,W.,
            Santibanez,J., Santos,R., Savery,G., Scherer,S., Shen,H., Shen,Y.,
            Sisson,I., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R.,
            Svatek,A., Taylor,E., Taylor,T., Thomas,N., Thorn,R., Thornton,R.,
            Trejos,Z., Usmani,K., Vargo,C., Verduzco,D., Villasana,D., Virk,D.,
            Volkov,A., Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,J.,
            Wei,X., Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R.,
            Wu,J., Yakub,S., Yan,K., Yuan,Y., Yu,F., Zhang,J., Zhang,L.,
            Zhang,Z., Zhou,J., Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 211176)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-NOV-2005) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 211176)
  AUTHORS   .
  CONSRTM   Bovine Genome Sequencing Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-2006) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Feb 9, 2006 this sequence version replaced gi:82734345.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
```

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table.
-------------- Genome Center
    Center: Baylor College of Medicine
    Center code: BCM
    Web site: http://www.hgsc.bcm.tmc.edu/
    Contact: hgsc-help@bcm.tmc.edu
-------------- Project Information
    Center project name: FKIF
    Center clone name: CH240-138G11
-------------- Summary Statistics
    Assembly program: Atlas 3.0;
    Consensus quality: 206639 bases at least Q40
    Consensus quality: 207886 bases at least Q30
    Consensus quality: 209008 bases at least Q20
    Estimated insert size: 211122; sum-of-contigs estimation
    Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
--------------
* NOTE: Estimated insert size may differ from sequence length
*   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*        1     4088: contig of 4088 bp in length
*     4089     4138: gap of 50 bp
*     4139     6488: contig of 2350 bp in length
*     6489     6538: gap of 50 bp
*     6539    33324: contig of 26786 bp in length
*    33325    33374: gap of 50 bp
*    33375    61001: contig of 27627 bp in length
*    61002    61051: gap of 50 bp
*    61052    70748: contig of 9697 bp in length
*    70749    70798: gap of 50 bp
*    70799    72915: contig of 2117 bp in length
*    72916    73015: gap of unknown length
*    73016    74193: contig of 1178 bp in length
*    74194    74489: gap of 296 bp
*    74490    81463: contig of 6974 bp in length
*    81464    81600: gap of 137 bp
*    81601    92734: contig of 11134 bp in length
*    92735    92784: gap of 50 bp
*    92785   137209: contig of 44425 bp in length
*   137210   137259: gap of 50 bp
*   137260   144851: contig of 7592 bp in length
*   144852   144973: gap of 122 bp
*   144974   158531: contig of 13558 bp in length
*   158532   158581: gap of 50 bp
*   158582   181513: contig of 22932 bp in length
*   181514   181613: gap of unknown length
*   181614   182633: contig of 1020 bp in length
*   182634   182733: gap of unknown length
*   182734   183805: contig of 1072 bp in length
*   183806   183905: gap of unknown length
*   183906   185785: contig of 1880 bp in length
*   185786   185885: gap of unknown length
*   185886   211176: contig of 25291 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
                     /clone="CH240-138G11"
     gap             4089. .4138
                     /estimated_length=50
     gap             6489. .6538
                     /estimated_length=50
     gap             33325. .33374
                     /estimated_length=50
     gap             61002. .61051
                     /estimated_length=50
     gap             70749. .70798
                     /estimated_length=50
     gap             72916. .73015
                     /estimated_length=unknown
     gap             74194. .74489
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     gap             81464. .81600
                     /estimated_length=137
     gap             92735. .92784
                     /estimated_length=50
     gap             137210. .137259
                     /estimated_length=50
     gap             144852. .144973
                     /estimated_length=122
     gap             158532. .158581
                     /estimated_length=50
     gap             181514. .181613
                     /estimated_length=unknown
     gap             182634. .182733
                     /estimated_length=unknown
     gap             183806. .183905
                     /estimated_length=unknown
     gap             185786. .185885
                     /estimated_length=unknown
ORIGIN

  Query Match             100.0%;  Score 17;  DB 12;  Length 211176;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db     103111 CGCATCTCCCACCCCCA 103095


RESULT 66
AC095947/c
LOCUS       AC095947              220629 bp    DNA     linear   HTG 09-SEP-2004
DEFINITION  Rattus norvegicus clone CH230-11A9, *** SEQUENCING IN PROGRESS ***,
            6 ordered pieces.
ACCESSION   AC095947
VERSION     AC095947.12  GI:51948547
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 220629)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Pan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
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            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., Mcleod,M., Mcneill,T., Meenen,E., Milosavljevic,A.,
            Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
            Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
            Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G.,
            Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
            Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A.,
            Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E.,
            Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
            Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A.,
            Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,
            Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,
            Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,
            Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,
            Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
            Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,
            Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
            Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R.,
            Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
            Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
            Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
            Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 220629)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 220629)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-SEP-2004) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 9, 2004 this sequence version replaced gi:24940730.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help.tmc.edu
            -------------- Project Information
                Center project name: GDYD
                Center clone name: CH230-11A9
            -------------- Summary Statistics
                Sequencing vector: Plasmid;
                Chemistry: Dye-terminator Big Dye: 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 222943 bases at least Q40
                Consensus quality: 223584 bases at least Q30
                Consensus quality: 223929 bases at least Q20
                Estimated insert size: 119540; sum-of-contigs estimation
                Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
            * The sequence data in this record represents an 'enhanced' version
            * of a Phase 2 submission.  The indicated order and orientation of
            * each sequence has been established using one or more of the
            * following: read-pair data from individual subclones, overlaps
            * with neighboring clones, alignment with available reference
            * sequence (e.g., human), and/or confirmation by PCR testing.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    28593: contig of 28593 bp in length
            *    28594    28990: gap of 397 bp
            *    28991    38766: contig of 9776 bp in length
            *    38767    38915: gap of 149 bp
            *    38916   125423: contig of 86508 bp in length
            *   125424   125525: gap of 102 bp
            *   125526   193004: contig of 67479 bp in length
            *   193005   194511: gap of 1507 bp
            *   194512   205308: contig of 10797 bp in length
            *   205309   205396: gap of 88 bp
            *   205397   220629: contig of 15233 bp in length.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-11A9"
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                     /note="assembly_name:gap"
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                     /estimated_length=397
     misc_feature    28991. .38766
                     /note="assembly_name:Contig40"
     misc_feature    38767. .38915
                     /note="assembly_name:gap"
     gap             38767. .38915
                     /estimated_length=149
     misc_feature    38916. .125423
                     /note="assembly_name:Contig46"
     misc_feature    125424. .125525
                     /note="assembly_name:gap"
     gap             125424. .125525
                     /estimated_length=102
     misc_feature    125526. .193004
                     /note="assembly_name:Contig47"
     misc_feature    193005. .194511
                     /note="assembly_name:gap"
     gap             193005. .194511
                     /estimated_length=1507
     misc_feature    194512. .205308
                     /note="assembly_name:Contig39"
     misc_feature    205309. .205396
                     /note="assembly_name:gap"
     gap             205309. .205396
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     misc_feature    205397. .220629
                     /note="assembly_name:Contig45"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 12;  Length 220629;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db      34515 CGCATCTCCCACCCCCA 34499


RESULT 67
AC104517
LOCUS       AC104517              253108 bp    DNA     linear   HTG 15-MAY-2002
DEFINITION  Mus musculus strain C57BL6/J clone RP23-76P8, WORKING DRAFT
            SEQUENCE, 20 unordered pieces.
ACCESSION   AC104517
VERSION     AC104517.3  GI:18092978
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 253108)
  AUTHORS   Grills,G., Li,L., Montgomery,K.T., Brown,W.A., Chiu,D., Decker,J.,
            Fusina,M., Haider,A., Keller,A., Perera,A., Shim,C., Thomas,E.,
            Zencheck,W., Xi,C., Juels,P. and Kucherlapati,R.
  TITLE     High Throughput Mouse Sequencing
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 253108)
  AUTHORS   Grills,G., Li,L., Montgomery,K.T., Brown,W.A., Chiu,D., Decker,J.,
            Fusina,M., Haider,A., Keller,A., Perera,A., Shim,C., Thomas,E.,
            Zencheck,W., Xi,C., Juels,P. and Kucherlapati,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-DEC-2001) Harvard Partners Center for Genetics and
            Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
            02139, USA
COMMENT     On Jan 9, 2002 this sequence version replaced gi:17976444.
            ----------Genome Center
            Center:  Harvard Partners Genome Center
            Center Code:  HPGC
            Web site: http://www.hpcgg.org/Sequence/mouse.html
            Contact: hpgc@mendel.mgh.harvard.edu
            ----------Summary Statistics
            Center project name:  AFF
            Sequencing vector:  pSMART; AF399742
            Chemistry:  Dye-terminator Big Dye; 100%
            *Consensus quality:  243677 at least Q20
            *Consensus quality:  242058 at least Q30
            *Consensus quality:  239529 at least Q40
            Estimated insert size:   agarose-FP - N/A
            **Estimated insert size: 252728 - sum-of-contigs
            Quality coverage:  agarose-FP - N/A
            Quality coverage:  7.7 x in Q20 bases; sum-of-contigs estimation
            ----------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 20 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    65522: contig of 65522 bp in length
            *   65523    65542: gap of unknown length
            *   65543   116856: contig of 51314 bp in length
            *  116857   116876: gap of unknown length
            *  116877   147216: contig of 30340 bp in length
            *  147217   147236: gap of unknown length
            *  147237   168381: contig of 21145 bp in length
            *  168382   168401: gap of unknown length
            *  168402   185362: contig of 16961 bp in length
            *  185363   185382: gap of unknown length
            *  185383   196248: contig of 10866 bp in length
            *  196249   196268: gap of unknown length
            *  196269   203440: contig of 7172 bp in length
            *  203441   203460: gap of unknown length
            *  203461   210414: contig of 6954 bp in length
            *  210415   210434: gap of unknown length
            *  210435   217990: contig of 7556 bp in length
            *  217991   218010: gap of unknown length
            *  218011   223672: contig of 5662 bp in length
            *  223673   223692: gap of unknown length
            *  223693   228419: contig of 4727 bp in length
            *  228420   228439: gap of unknown length
            *  228440   232446: contig of 4007 bp in length
            *  232447   232466: gap of unknown length
            *  232467   237298: contig of 4832 bp in length
            *  237299   237318: gap of unknown length
            *  237319   241393: contig of 4075 bp in length
            *  241394   241413: gap of unknown length
            *  241414   244210: contig of 2797 bp in length
            *  244211   244230: gap of unknown length
            *  244231   245725: contig of 1495 bp in length
            *  245726   245745: gap of unknown length
            *  245746   247478: contig of 1733 bp in length
            *  247479   247498: gap of unknown length
            *  247499   249821: contig of 2323 bp in length
            *  249822   249841: gap of unknown length
            *  249842   251937: contig of 2096 bp in length
            *  251938   251957: gap of unknown length
            *  251958   253108: contig of 1151 bp in length.
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                     /mol_type="genomic DNA"
                     /strain="C57BL6/J"
                     /db_xref="taxon:10090"
                     /clone="RP23-76P8"
                     /sex="male"
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ORIGIN

  Query Match             100.0%;  Score 17;  DB 12;  Length 253108;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db     204275 CGCATCTCCCACCCCCA 204291


RESULT 68
AC115671
LOCUS       AC115671               266673 bp    DNA     linear   HTG 15-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-79B11, *** SEQUENCING IN PROGRESS
            ***, 2 unordered pieces.
ACCESSION   AC115671
VERSION     AC115671.8  GI:25013214
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 266673)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
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            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 266673)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 266673)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 15, 2002 this sequence version replaced gi:23269814.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GUGA
                Center clone name: CH230-79B11
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 245643 bases at least Q40
                Consensus quality: 248735 bases at least Q30
                Consensus quality: 250802 bases at least Q20
                Estimated insert size: 255989; sum-of-contigs estimation
                Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
            * NOTE: This sequence may represent more than one clone.
            * NOTE: This is a 'working draft' sequence. It currently
```

```
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1   265069: contig of 265069 bp in length
            *   265070   265169: gap of unknown length
            *   265170   266673: contig of 1504 bp in length.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-79B11"
     misc_feature    1. .1537
                     /note="wgs_contig"
     misc_feature    1588. .3374
                     /note="wgs_contig"
     misc_feature    145070. .146665
                     /note="wgs_contig"
     misc_feature    262641. .265069
                     /note="wgs_contig"
     gap             265070. .265169
                     /estimated_length=unknown
ORIGIN

  Query Match             100.0%;  Score 17;  DB 12;  Length 266673;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db      58772 CGCATCTCCCACCCCCA 58788


RESULT 69
AC163875/c
LOCUS       AC163875               308565 bp    DNA     linear   HTG 01-JUL-2005
DEFINITION  Bos taurus clone CH240-138G9, *** SEQUENCING IN PROGRESS ***, 49
            unordered pieces.
ACCESSION   AC163875
VERSION     AC163875.2  GI:68300255
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 308565)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
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            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 308565)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2005) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 308565)
  AUTHORS   Cow Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jun 29, 2005 this sequence version replaced gi:67625877.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: FIAJ
                Center clone name: CH240-138G9
            -------------- Summary Statistics
                Assembly program: Atlas 3.0;
                Consensus quality: 285100 bases at least Q40
                Consensus quality: 289762 bases at least Q30
                Consensus quality: 293819 bases at least Q20
                Estimated insert size: 292813; sum-of-contigs estimation
                Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
            * NOTE: This sequence may represent more than one clone.
```

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* NOTE: This is a ''working draft' sequence. It currently
* consists of 49 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*     7092     7191: gap of unknown length
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*     9532    10266: gap of 735 bp
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*    57086    58972: contig of 1887 bp in length
*    58973    60160: gap of 1188 bp
*    60161    64139: contig of 3979 bp in length
*    64140    64189: gap of 50 bp
*    64190    74634: contig of 10445 bp in length
*    74635    74825: gap of 191 bp
*    74826    83896: contig of 9071 bp in length
*    83897    83946: gap of 50 bp
*    83947   100514: contig of 16568 bp in length
*   100515   100564: gap of 50 bp
*   100565   107507: contig of 6943 bp in length
*   107508   107557: gap of 50 bp
*   107558   110097: contig of 2540 bp in length
*   110098   110238: gap of 141 bp
*   110239   127812: contig of 17574 bp in length
*   127813   127862: gap of 50 bp
*   127863   153487: contig of 25625 bp in length
*   153488   153537: gap of 50 bp
*   153538   156272: contig of 2735 bp in length
*   156273   157724: gap of 1452 bp
*   157725   171303: contig of 13579 bp in length
*   171304   172125: gap of 822 bp
*   172126   176677: contig of 4552 bp in length
*   176678   176777: gap of unknown length
*   176778   203635: contig of 26858 bp in length
*   203636   204021: gap of 386 bp
*   204022   207442: contig of 3421 bp in length
*   207443   207635: gap of 193 bp
*   207636   220100: contig of 12465 bp in length
*   220101   220150: gap of 50 bp
*   220151   224458: contig of 4308 bp in length
*   224459   224508: gap of 50 bp
*   224509   237679: contig of 13171 bp in length
*   237680   237729: gap of 50 bp
*   237730   239586: contig of 1857 bp in length
*   239587   239636: gap of 50 bp
*   239637   245112: contig of 5476 bp in length
*   245113   245626: gap of 514 bp
*   245627   247299: contig of 1673 bp in length
*   247300   247399: gap of unknown length
*   247400   250678: contig of 3279 bp in length
*   250679   251058: gap of 380 bp
*   251059   252760: contig of 1702 bp in length
*   252761   252810: gap of 50 bp
*   252811   254877: contig of 2067 bp in length
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*   254978   257889: contig of 2912 bp in length
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*   261118   262480: contig of 1363 bp in length
*   262481   262836: gap of 356 bp
*   262837   265513: contig of 2677 bp in length
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Job time : 1960 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: July 3, 2006, 06:14:00 ; Search time 287 Seconds
(without alignments)
412.990 Million cell updates/sec

Title: US-10-615-497-9
Perfect score: 17
Sequence: 1 cgcatctcccacccca 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 92

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : N_Geneseq_8:*
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2: geneseqn1990s:*
3: geneseqn2000s:*
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5: geneseqn2001bs:*
6: geneseqn2002as:*
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9: geneseqn2003bs:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	100.0	17	12	ADO03974	Ado03974 Human CYP
2	17	100.0	24	12	ADJ14473	Adj14473 Debrisoqu
3	17	100.0	24	12	ADO60575	Ado60575 Human deb
4	17	100.0	24	14	AEC89739	Aec89739 CYP2D6 ge
5	17	100.0	25	12	ADJ14503	Adj14503 Debrisoqu
6	17	100.0	25	12	ADJ14724	Adj14724 Debrisoqu
7	17	100.0	25	12	ADO60605	Ado60605 Human deb
8	17	100.0	25	12	ADO60907	Ado60907 Human deb
9	17	100.0	25	12	ADO60827	Ado60827 Human deb
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11	17	100.0	25	14	AEC89769	Aec89769 CYP2D6 ge
12	17	100.0	25	14	AEC89991	Aec89991 CYP2D6 ge
13	17	100.0	41	14	AEC32583	Aec32583 Human cyt
14	17	100.0	42	12	ADJ14690	Adj14690 Debrisoqu
15	17	100.0	42	12	ADJ14689	Adj14689 Debrisoqu
16	17	100.0	42	12	ADO60792	Ado60792 Human deb
17	17	100.0	42	12	ADO60791	Ado60791 Human deb
18	17	100.0	42	14	AEC89956	Aec89956 CYP2D6 ge
19	17	100.0	42	14	AEC89955	Aec89955 CYP2D6 ge
c 20	17	100.0	43	12	ADJ14477	Adj14477 Debrisoqu
c 21	17	100.0	43	12	ADJ14476	Adj14476 Debrisoqu
c 22	17	100.0	43	12	ADO60579	Ado60579 Human deb
c 23	17	100.0	43	12	ADO60578	Ado60578 Human deb
c 24	17	100.0	43	14	AEC89742	Aec89742 CYP2D6 ge
c 25	17	100.0	43	14	AEC89743	Aec89743 CYP2D6 ge
c 26	17	100.0	44	12	ADJ14728	Adj14728 Debrisoqu
c 27	17	100.0	44	12	ADJ14507	Adj14507 Debrisoqu
c 28	17	100.0	44	12	ADJ14506	Adj14506 Debrisoqu
c 29	17	100.0	44	12	ADJ14727	Adj14727 Debrisoqu
c 30	17	100.0	44	12	ADO60609	Ado60609 Human deb
c 31	17	100.0	44	12	ADO60911	Ado60911 Human deb
c 32	17	100.0	44	12	ADO60608	Ado60608 Human deb
c 33	17	100.0	44	12	ADO60910	Ado60910 Human deb
c 34	17	100.0	44	12	ADO60830	Ado60830 Human deb
c 35	17	100.0	44	12	ADO60831	Ado60831 Human deb
c 36	17	100.0	44	14	AEC90075	Aec90075 CYP2D6 ge
c 37	17	100.0	44	14	AEC89995	Aec89995 CYP2D6 ge
c 38	17	100.0	44	14	AEC89994	Aec89994 CYP2D6 ge
c 39	17	100.0	44	14	AEC90074	Aec90074 CYP2D6 ge
c 40	17	100.0	44	14	AEC89773	Aec89773 CYP2D6 ge
c 41	17	100.0	44	14	AEC89772	Aec89772 CYP2D6 ge
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43	17	100.0	51	6	ABK30188	Abk30188 CYP2D6 ge
44	17	100.0	51	6	ABK30182	Abk30182 CYP2D6 ge
45	17	100.0	51	6	ABK30181	Abk30181 CYP2D6 ge
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49	17	100.0	347	15	AEF35799	Aef35799 Human cyt
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52	17	100.0	483	12	ADO84826	Ado84826 CYP2 plas
53	17	100.0	483	14	AEC32560	Aec32560 Plasmid C
54	17	100.0	484	12	ADO84825	Ado84825 CYP2 plas
55	17	100.0	484	14	AEC32559	Aec32559 Plasmid C
56	17	100.0	490	8	ABT33980	Abt33980 Human pig
57	17	100.0	490	10	ADC26791	Adc26791 Human lip
58	17	100.0	500	15	AEE02739	Aee02739 Human Cyt
59	17	100.0	500	15	AEE02740	Aee02740 Human Cyt
60	17	100.0	652	12	ADO84823	Ado84823 CYP2 plas
61	17	100.0	652	12	ADO84824	Ado84824 CYP2 plas
62	17	100.0	652	14	AEC32557	Aec32557 Plasmid C
63	17	100.0	652	14	AEC32558	Aec32558 Plasmid C
64	17	100.0	901	12	ADM94996	Adm94996 Human cyt
65	17	100.0	1190	8	ABT33976	Abt33976 Human pig
66	17	100.0	1190	10	ADC26818	Adc26818 Human lip
67	17	100.0	1450	4	AAD09849	Aad09849 Human CYP
68	17	100.0	2170	8	ABT33964	Abt33964 Human pig
69	17	100.0	2170	8	ABT33965	Abt33965 Human pig
70	17	100.0	4375	12	ADJ78569	Adj78569 Human cyt
71	17	100.0	4375	12	ADM28897	Adm28897 Human pse
72	17	100.0	4500	8	ADB25775	Adb25775 Human CYP
c 73	17	100.0	6001	13	ADS89487	Ads89487 Oligonucl
c 74	17	100.0	6001	13	ADS89113	Ads89113 Human CYP
75	17	100.0	6472	6	ABQ72215	Abq72215 Human CYP
76	17	100.0	6472	6	ABQ72364	Abq72364 Human CYP
77	17	100.0	9432	6	AAD34213	Aad34213 Human cyt
78	17	100.0	9432	10	ACA61301	Aca61301 Human cyt
79	17	100.0	9432	12	ADF83400	Adf83400 Human CYP
80	17	100.0	9432	12	ADJ78563	Adj78563 Human cyt
81	17	100.0	9432	12	ADM28891	Adm28891 Human wil
82	17	100.0	9432	15	AEF35804	Aef35804 Human cyt
83	17	100.0	9432	15	AEF38201	Aef38201 Human deb
84	17	100.0	9433	10	ACA61302	Aca61302 Human cyt
85	17	100.0	9609	14	ADX00827	Adx00827 Human CYP
86	17	100.0	13278	12	ADJ78567	Adj78567 Human cyt
87	17	100.0	13278	12	ADM28895	Adm28895 Human pse
88	17	100.0	13677	12	ADJ78568	Adj78568 Human cyt
89	17	100.0	13677	12	ADM28896	Adm28896 Human pse
90	17	100.0	17060	12	ADJ78566	Adj78566 Human cyt
91	17	100.0	17060	12	ADM28894	Adm28894 Human pse

92 17 100.0 18000 15 AEF35808 Aef35808 Human cyt

ALIGNMENTS

RESULT 1
ADO03974
ID ADO03974 standard; DNA; 17 BP.
XX
AC ADO03974;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human CYP2D6 gene polymorphism detecting PCR primer, SNP11.
XX
KW Cytochrome P450 2D6; CYP2D6; polymorphism detection;
KW single nucleotide polymorphism; respiratory system; cystic fibrosis;
KW asthma; bronchitis; adult respiratory distress syndrome;
KW digestive system; cancer; inflammatory bowel disease; Crohn's disease;
KW pancreatitis; skeletal system; rheumatoid arthritis; osteoporosis;
KW spinal muscular atrophy; autoimmune disease; multiple sclerosis;
KW psoriasis; insulin dependent diabetes mellitus;
KW systemic lupus erythematosus; autoimmune haemolytic anaemia;
KW neurological disorder; Alzheimer's disease; Parkinson's disease;
KW schizophrenia; leukaemia; aging; human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2004091909-A1.
XX
PD 13-MAY-2004.
XX
PF 07-JUL-2003; 2003US-00615497.
XX
PR 05-JUL-2002; 2002US-0393967P.
PR 16-JUL-2002; 2002US-0396618P.
XX
PA (HUAN/) HUANG D H.
XX
PI Huang DH;
XX
DR WPI; 2004-374942/35.
XX
PT Identifying pre-selected polymorphisms present in cytochrome P450 2D6
PT gene sequences in samples, by generating a labeled nucleic acid and
PT relating labeled nucleic acid to identity of polymorphism.
XX
PS Claim 3; SEQ ID NO 9; 27pp; English.
XX
CC The invention relates to methods for identifying several pre-selected
CC polymorphisms present in cytochrome P450 2D6 (CYP2D6) gene. The method is
CC useful for identifying pre-selected polymorphisms present in cytochrome
CC P450 2D6 gene sequence, e.g., duplication, deletion, inversion,
CC insertion, translocation, polymorphism resulting in aberrant RNA splicing
CC and a single nucleotide polymorphism. It is useful for selecting a
CC therapeutic drug or its prodrug to treat a subject suffering from a
CC disease or disorder that involves the respiratory system (cystic
CC fibrosis, asthma, bronchitis and adult respiratory distress syndrome),
CC digestive system (cancers, inflammatory bowel disease, Crohn's disease
CC and pancreatitis), skeletal system (rheumatoid arthritis, osteoporosis
CC and spinal muscular atrophy), autoimmune disease (multiple sclerosis,
CC psoriasis, insulin dependent diabetes mellitus, systemic lupus
CC erythematosus and autoimmune haemolytic anaemia), neurological disorders
CC (Alzheimer's disease, Parkinson's disease and schizophrenia), various
CC leukaemias and aging. The present sequence is a PCR primer used for
CC detecting human CYP2D6 gene polymorphism. This sequence is used to
CC illustrate the method of the invention.
XX
SQ Sequence 17 BP; 3 A; 11 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 1 CGCATCTCCCACCCCCA 17

RESULT 2
ADJ14473
ID ADJ14473 standard; DNA; 24 BP.
XX
AC ADJ14473;
XX
DT 20-MAY-2004 (first entry)
XX
DE Debrisoquine 4-hydroxylase (CYP2D6)-related Invader oligo - SEQ ID 36.
XX
KW SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; Invader.
XX
OS Unidentified.
XX
PN US2003235848-A1.
XX
PD 25-DEC-2003.
XX
PF 11-APR-2003; 2003US-00411954.
XX
PR 11-APR-2002; 2002US-0371819P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
XX
PI Neville M, Indig MDA;
XX
DR WPI; 2004-070577/07.
XX
PT Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT with the primer set and detecting at least one of the footprint regions
PT with the assay probe.
XX
PS Example 3; SEQ ID NO 36; 55pp; English.
XX
CC The invention relates to a novel method for characterising a cytochrome
CC p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC comprises providing a sample with at least Y target sequences, a primer
CC set comprising a forward and a reverse primer sequence for each of the Y
CC target sequences and at least one assay probe configured to detect a
CC footprint region, amplifying the Y target sequences with the primer set
CC and detecting at least one of the footprint regions with the assay probe.
CC The method of the invention may be useful for characterising a cytochrome
CC p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC (cytochrome p450 2D6; CYP2D6)-related Invader oligonucleotide of the
CC invention.
XX
SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 7 CGCATCTCCCACCCCCA 23

RESULT 3
ADO60575
ID ADO60575 standard; DNA; 24 BP.
XX
AC ADO60575;
XX
DT 12-AUG-2004 (first entry)

XX
DE Human debrisoquine 4-hydroxylase, CYP2D6 invader oligonucleotide #8.
XX
KW oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW cytochrome p450; human; invader; ss.
XX
OS Homo sapiens.
XX
PN US2004096874-A1.
XX
PD 20-MAY-2004.
XX
PF 10-JUL-2003; 2003US-00617070.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2004-447680/42.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT associated polymorphisms.
XX
PS Example 3; SEQ ID NO 36; 172pp; English.
XX
CC The invention relates to a kit which comprises an oligonucleotide
CC detection assay configured for detecting the number of debrisoquine 4-
CC hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC identify the presence or absence of at least two CYP2D6 associated
CC polymorphisms. The kit and methods are useful for characterising
CC cytochrome p450 genes and alleles or for developing and optimising
CC nucleic acid detection assays for use in basic research, clinical
CC research and for the development of clinical detection assays. The
CC present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC invader oligonucleotide.
XX
SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 7 CGCATCTCCCACCCCCA 23

RESULT 4
AEC89739
ID AEC89739 standard; DNA; 24 BP.
XX
AC AEC89739;
XX
DT 17-NOV-2005 (first entry)
XX
DE CYP2D6 gene-specific invader oligonucleotide - SEQ ID 36.
XX
KW DNA detection; SNP detection; CYP2D6; ss.
XX
OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 3; SEQ ID NO 36; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a CYP2D6-specific invader oligonucleotide
CC that was used in an example of the invention.
XX
SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 7 CGCATCTCCCACCCCCA 23

RESULT 5
ADJ14503
ID ADJ14503 standard; DNA; 25 BP.
XX
AC ADJ14503;
XX
DT 20-MAY-2004 (first entry)
XX
DE Debrisoquine 4-hydroxylase (CYP2D6)-related Invader oligo - SEQ ID 66.
XX
KW SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; Invader.
XX
OS Unidentified.
XX
PN US2003235848-A1.
XX
PD 25-DEC-2003.
XX
PF 11-APR-2003; 2003US-00411954.
XX
PR 11-APR-2002; 2002US-0371819P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
XX
PI Neville M, Indig MDA;
XX
DR WPI; 2004-070577/07.
XX

```
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 66; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related Invader oligonucleotide of the
CC   invention.
XX
SQ   Sequence 25 BP; 4 A; 15 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24


RESULT 6
ADJ14724
ID   ADJ14724 standard; DNA; 25 BP.
XX
AC   ADJ14724;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related Invader oligo - SEQ ID 288.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; Invader.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 288; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related Invader oligonucleotide of the
CC   invention.
XX
SQ   Sequence 25 BP; 4 A; 15 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24


RESULT 7
ADO60605
ID   ADO60605 standard; DNA; 25 BP.
XX
AC   ADO60605;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 invader oligonucleotide #14.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; invader; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 3; SEQ ID NO 66; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   invader oligonucleotide.
XX
SQ   Sequence 25 BP; 4 A; 15 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24
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RESULT 8
ADO60907
ID   ADO60907 standard; DNA; 25 BP.
XX
AC   ADO60907;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 invader oligonucleotide #54.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; invader; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 4; SEQ ID NO 368; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   invader oligonucleotide.
XX
SQ   Sequence 25 BP; 4 A; 15 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24


RESULT 9
ADO60827
ID   ADO60827 standard; DNA; 25 BP.
XX
AC   ADO60827;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 invader oligonucleotide #92.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; invader; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 3; SEQ ID NO 288; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   invader oligonucleotide.
XX
SQ   Sequence 25 BP; 4 A; 15 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24


RESULT 10
AEC90071
ID   AEC90071 standard; DNA; 25 BP.
XX
AC   AEC90071;
XX
DT   17-NOV-2005  (first entry)
XX
DE   CYP2D6 gene-specific invader oligonucleotide - SEQ ID 368.
XX
KW   DNA detection; SNP detection; CYP2D6; ss.
XX
OS   Unidentified.
XX
PN   US2005196771-A1.
XX
PD   08-SEP-2005.
XX
PF   01-OCT-2004; 2004US-00956507.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
PR   10-JUL-2003; 2003US-00617070.
PR   02-OCT-2003; 2003US-0508220P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
```

PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 4; SEQ ID NO 368; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a CYP2D6-specific invader oligonucleotide
CC that was used in an example of the invention.
XX
SQ Sequence 25 BP; 4 A; 15 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 8 CGCATCTCCCACCCCCA 24

RESULT 11
AEC89769
ID AEC89769 standard; DNA; 25 BP.
XX
AC AEC89769;
XX
DT 17-NOV-2005 (first entry)
XX
DE CYP2D6 gene-specific invader oligonucleotide - SEQ ID 66.
XX
KW DNA detection; SNP detection; CYP2D6; ss.
XX
OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 3; SEQ ID NO 66; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a CYP2D6-specific invader oligonucleotide
CC that was used in an example of the invention.
XX
SQ Sequence 25 BP; 4 A; 15 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 8 CGCATCTCCCACCCCCA 24

RESULT 12
AEC89991
ID AEC89991 standard; DNA; 25 BP.
XX
AC AEC89991;
XX
DT 17-NOV-2005 (first entry)
XX
DE CYP2D6 gene-specific invader oligonucleotide - SEQ ID 288.
XX
KW DNA detection; SNP detection; CYP2D6; ss.
XX
OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 3; SEQ ID NO 288; 189pp; English.
XX

```
CC   The invention comprises an oligonucleotide detection assay configured for
CC   detecting the number of CYP2D6 gene copies present in a sample, and
CC   configured for identifying the presence or absence of at least two CYP2D6
CC   -associated polymorphisms. The oligonucleotide detection assay of the
CC   invention is useful for genotyping a subject having a CYP2D6 gene. The
CC   present DNA sequence represents a CYP2D6-specific invader oligonucleotide
CC   that was used in an example of the invention.
XX
SQ   Sequence 25 BP; 4 A; 15 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24


RESULT 13
AEC32583
ID   AEC32583 standard; DNA; 41 BP.
XX
AC   AEC32583;
XX
DT   03-NOV-2005  (first entry)
XX
DE   Human cytochrome P450 CYP2 LDR oligonucleotide Z2D64MT.
XX
KW   ss; primer; detection; single nucleotide polymorphism; SNP; CYP2;
KW   cytochrome P450 2; diagnostic; cytochrome P450;
KW   isoform-specific polymer chain reaction; IS-PCR.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   DE102004006477-A1.
XX
PD   25-AUG-2005.
XX
PF   04-FEB-2004; 2004DE-10006477.
XX
PR   04-FEB-2004; 2004DE-10006477.
XX
PA   (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.
XX
PI   Neunaber R,  Strohner P,  Schreiber J,  Voigt G;
XX
DR   WPI; 2005-592623/61.
XX
PT   Process for demonstrating the presence of single nucleotide polymorphism
PT   in human genes, comprises using a priming agent.
XX
PS   Claim 1; SEQ ID NO 73; 77pp; German.
XX
CC   This invention describes a novel method of detecting the presence of
CC   single nucleotide polymorphisms (SNPs) in human CYP2-genes using a
CC   priming agent and/or a probe, where the priming agent effects high-
CC   resolution amplification of the respective CYP2 allelomorph. The method
CC   can be incorporated into a diagnostic kit that detects the presence of
CC   polymorphisms in human cytochrome P450 genes comprising a synthetic
CC   oligonucleotide that amplifies isoform-specific (IS-PCR) polymer chain
CC   reactions using a DNA polymerase chain reaction. The kit components
CC   selectively immobilize single-stranded biotinized IS-PCR products on
CC   streptavidin-coated micro-titration slides under stable thermal
CC   conditions. Test-optimized, allelmorph-specific, fluorescein
CC   isothiocyanate (FITC)-marked synthetic oligonucleotides facilitate
CC   accurate identification of the genotype of the immobilized amplification
CC   products through a sequence of hybridization, subsequent washing and
CC   detection by fluorometry or photometry. The novel diagnostic process is
CC   rapid and cost-effective. This sequence represents a primer used to
CC   detect a SNP in the human cytochrome P450 CYP2 gene.
XX
SQ   Sequence 41 BP; 8 A; 20 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 14;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         24 CGCATCTCCCACCCCCA 40


RESULT 14
ADJ14690
ID   ADJ14690 standard; DNA; 42 BP.
XX
AC   ADJ14690;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 253.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 253; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC   invention.
XX
SQ   Sequence 42 BP; 6 A; 23 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          1 CGCATCTCCCACCCCCA 17


RESULT 15
ADJ14689
ID   ADJ14689 standard; DNA; 42 BP.
```

```
XX
AC   ADJ14689;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 252.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 252; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC   invention.
XX
SQ   Sequence 42 BP; 7 A; 23 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          1 CGCATCTCCCACCCCCA 17


RESULT 16
ADO60792
ID   ADO60792 standard; DNA; 42 BP.
XX
AC   ADO60792;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #98.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 3; SEQ ID NO 253; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   target.
XX
SQ   Sequence 42 BP; 6 A; 23 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          1 CGCATCTCCCACCCCCA 17


RESULT 17
ADO60791
ID   ADO60791 standard; DNA; 42 BP.
XX
AC   ADO60791;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #97.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
```

PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT associated polymorphisms.
XX
PS Example 3; SEQ ID NO 252; 172pp; English.
XX
CC The invention relates to a kit which comprises an oligonucleotide
CC detection assay configured for detecting the number of debrisoquine 4-
CC hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC identify the presence or absence of at least two CYP2D6 associated
CC polymorphisms. The kit and methods are useful for characterising
CC cytochrome p450 genes and alleles or for developing and optimising
CC nucleic acid detection assays for use in basic research, clinical
CC research and for the development of clinical detection assays. The
CC present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC target.
XX
SQ Sequence 42 BP; 7 A; 23 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 1 CGCATCTCCCACCCCCA 17

RESULT 18
AEC89956
ID AEC89956 standard; DNA; 42 BP.
XX
AC AEC89956;
XX
DT 17-NOV-2005 (first entry)
XX
DE CYP2D6 gene target region - SEQ ID 253.
XX
KW DNA detection; SNP detection; CYP2D6; ds.
XX
OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 3; SEQ ID NO 253; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a target region of the CYP2D6 gene which
CC was used in an example of the invention.
XX
SQ Sequence 42 BP; 6 A; 23 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 1 CGCATCTCCCACCCCCA 17

RESULT 19
AEC89955
ID AEC89955 standard; DNA; 42 BP.
XX
AC AEC89955;
XX
DT 17-NOV-2005 (first entry)
XX
DE CYP2D6 gene target region - SEQ ID 252.
XX
KW DNA detection; SNP detection; CYP2D6; ds.
XX
OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 3; SEQ ID NO 252; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a target region of the CYP2D6 gene which
CC was used in an example of the invention.
XX
SQ Sequence 42 BP; 7 A; 23 C; 6 G; 6 T; 0 U; 0 Other;

```
  Query Match           100.0%;  Score 17;  DB 14;  Length 42;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          1 CGCATCTCCCACCCCCA 17


RESULT 20
ADJ14477/c
ID   ADJ14477 standard; DNA; 43 BP.
XX
AC   ADJ14477;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 40.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 40; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC   invention.
XX
SQ   Sequence 43 BP; 7 A; 4 C; 26 G; 6 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 17;  DB 12;  Length 43;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 21
ADJ14476/c
ID   ADJ14476 standard; DNA; 43 BP.
XX
AC   ADJ14476;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 39.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 39; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC   invention.
XX
SQ   Sequence 43 BP; 7 A; 5 C; 26 G; 5 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 17;  DB 12;  Length 43;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 22
ADO60579/c
ID   ADO60579 standard; DNA; 43 BP.
XX
AC   ADO60579;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #16.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
```

```
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 3; SEQ ID NO 40; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   target.
XX
SQ   Sequence 43 BP; 7 A; 4 C; 26 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 23
ADO60578/c
ID   ADO60578 standard; DNA; 43 BP.
XX
AC   ADO60578;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #15.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 3; SEQ ID NO 39; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   target.
XX
SQ   Sequence 43 BP; 7 A; 5 C; 26 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 24
AEC89742/c
ID   AEC89742 standard; DNA; 43 BP.
XX
AC   AEC89742;
XX
DT   17-NOV-2005  (first entry)
XX
DE   CYP2D6 gene target region - SEQ ID 39.
XX
KW   DNA detection; SNP detection; CYP2D6; ds.
XX
OS   Unidentified.
XX
PN   US2005196771-A1.
XX
PD   08-SEP-2005.
XX
PF   01-OCT-2004; 2004US-00956507.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
PR   10-JUL-2003; 2003US-00617070.
PR   02-OCT-2003; 2003US-0508220P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
PA   (CAOF/) CAO F.
PA   (OLDE/) OLDENBURG M C.
PA   (KOEL/) KOELBL J A.
PA   (AIZE/) AIZENSTEIN B D.
PA   (DAVE/) DAVEY K.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2005-637912/65.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies and for identifying the presence or absence
PT   of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT   having a CYP2D6 gene.
XX
PS   Example 3; SEQ ID NO 39; 189pp; English.
XX
CC   The invention comprises an oligonucleotide detection assay configured for
```

```
CC   detecting the number of CYP2D6 gene copies present in a sample, and
CC   configured for identifying the presence or absence of at least two CYP2D6
CC   -associated polymorphisms. The oligonucleotide detection assay of the
CC   invention is useful for genotyping a subject having a CYP2D6 gene. The
CC   present DNA sequence represents a target region of the CYP2D6 gene which
CC   was used in an example of the invention.
XX
SQ   Sequence 43 BP; 7 A; 5 C; 26 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 14;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 25
AEC89743/c
ID   AEC89743 standard; DNA; 43 BP.
XX
AC   AEC89743;
XX
DT   17-NOV-2005  (first entry)
XX
DE   CYP2D6 gene target region - SEQ ID 40.
XX
KW   DNA detection; SNP detection; CYP2D6; ds.
XX
OS   Unidentified.
XX
PN   US2005196771-A1.
XX
PD   08-SEP-2005.
XX
PF   01-OCT-2004; 2004US-00956507.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
PR   10-JUL-2003; 2003US-00617070.
PR   02-OCT-2003; 2003US-0508220P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
PA   (CAOF/) CAO F.
PA   (OLDE/) OLDENBURG M C.
PA   (KOEL/) KOELBL J A.
PA   (AIZE/) AIZENSTEIN B D.
PA   (DAVE/) DAVEY K.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2005-637912/65.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies and for identifying the presence or absence
PT   of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT   having a CYP2D6 gene.
XX
PS   Example 3; SEQ ID NO 40; 189pp; English.
XX
CC   The invention comprises an oligonucleotide detection assay configured for
CC   detecting the number of CYP2D6 gene copies present in a sample, and
CC   configured for identifying the presence or absence of at least two CYP2D6
CC   -associated polymorphisms. The oligonucleotide detection assay of the
CC   invention is useful for genotyping a subject having a CYP2D6 gene. The
CC   present DNA sequence represents a target region of the CYP2D6 gene which
CC   was used in an example of the invention.
XX
SQ   Sequence 43 BP; 7 A; 4 C; 26 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 14;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 26
ADJ14728/c
ID   ADJ14728 standard; DNA; 44 BP.
XX
AC   ADJ14728;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 292.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 292; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC   invention.
XX
SQ   Sequence 44 BP; 7 A; 5 C; 27 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 27
ADJ14507/c
ID   ADJ14507 standard; DNA; 44 BP.
XX
AC   ADJ14507;
```

```
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 70.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 70; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC   invention.
XX
SQ   Sequence 44 BP; 7 A; 5 C; 27 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 28
ADJ14506/c
ID   ADJ14506 standard; DNA; 44 BP.
XX
AC   ADJ14506;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 69.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
XX
PS   Example 3; SEQ ID NO 69; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC   invention.
XX
SQ   Sequence 44 BP; 7 A; 4 C; 27 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 29
ADJ14727/c
ID   ADJ14727 standard; DNA; 44 BP.
XX
AC   ADJ14727;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 291.
XX
KW   SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW   debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS   Unidentified.
XX
PN   US2003235848-A1.
XX
PD   25-DEC-2003.
XX
PF   11-APR-2003; 2003US-00411954.
XX
PR   11-APR-2002; 2002US-0371819P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
XX
PI   Neville M,  Indig MDA;
XX
DR   WPI; 2004-070577/07.
XX
PT   Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT   with the primer set and detecting at least one of the footprint regions
PT   with the assay probe.
```

```
XX
PS   Example 3; SEQ ID NO 291; 55pp; English.
XX
CC   The invention relates to a novel method for characterising a cytochrome
CC   p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC   comprises providing a sample with at least Y target sequences, a primer
CC   set comprising a forward and a reverse primer sequence for each of the Y
CC   target sequences and at least one assay probe configured to detect a
CC   footprint region, amplifying the Y target sequences with the primer set
CC   and detecting at least one of the footprint regions with the assay probe.
CC   The method of the invention may be useful for characterising a cytochrome
CC   p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC   (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC   invention.
XX
SQ   Sequence 44 BP; 7 A; 4 C; 27 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 30
ADO60609/c
ID   ADO60609 standard; DNA; 44 BP.
XX
AC   ADO60609;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #28.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 3; SEQ ID NO 70; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   target.
XX
SQ   Sequence 44 BP; 7 A; 5 C; 27 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 31
ADO60911/c
ID   ADO60911 standard; DNA; 44 BP.
XX
AC   ADO60911;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #104.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 4; SEQ ID NO 372; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   target.
XX
SQ   Sequence 44 BP; 7 A; 5 C; 27 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 32
ADO60608/c
```

```
ID   ADO60608 standard; DNA; 44 BP.
XX
AC   ADO60608;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #27.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 3; SEQ ID NO 69; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   target.
XX
SQ   Sequence 44 BP; 7 A; 4 C; 27 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 33
ADO60910/c
ID   ADO60910 standard; DNA; 44 BP.
XX
AC   ADO60910;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #103.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT   associated polymorphisms.
XX
PS   Example 4; SEQ ID NO 371; 172pp; English.
XX
CC   The invention relates to a kit which comprises an oligonucleotide
CC   detection assay configured for detecting the number of debrisoquine 4-
CC   hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC   identify the presence or absence of at least two CYP2D6 associated
CC   polymorphisms. The kit and methods are useful for characterising
CC   cytochrome p450 genes and alleles or for developing and optimising
CC   nucleic acid detection assays for use in basic research, clinical
CC   research and for the development of clinical detection assays. The
CC   present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC   target.
XX
SQ   Sequence 44 BP; 7 A; 4 C; 27 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 34
ADO60830/c
ID   ADO60830 standard; DNA; 44 BP.
XX
AC   ADO60830;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase, CYP2D6 target #171.
XX
KW   oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW   cytochrome p450; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2004096874-A1.
XX
PD   20-MAY-2004.
XX
PF   10-JUL-2003; 2003US-00617070.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2004-447680/42.
```

XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT associated polymorphisms.
XX
PS Example 3; SEQ ID NO 291; 172pp; English.
XX
CC The invention relates to a kit which comprises an oligonucleotide
CC detection assay configured for detecting the number of debrisoquine 4-
CC hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC identify the presence or absence of at least two CYP2D6 associated
CC polymorphisms. The kit and methods are useful for characterising
CC cytochrome p450 genes and alleles or for developing and optimising
CC nucleic acid detection assays for use in basic research, clinical
CC research and for the development of clinical detection assays. The
CC present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC target.
XX
SQ Sequence 44 BP; 7 A; 4 C; 27 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 35
ADO60831/c
ID ADO60831 standard; DNA; 44 BP.
XX
AC ADO60831;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human debrisoquine 4-hydroxylase, CYP2D6 target #172.
XX
KW oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW cytochrome p450; human; ss.
XX
OS Homo sapiens.
XX
PN US2004096874-A1.
XX
PD 20-MAY-2004.
XX
PF 10-JUL-2003; 2003US-00617070.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2004-447680/42.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT associated polymorphisms.
XX
PS Example 3; SEQ ID NO 292; 172pp; English.
XX
CC The invention relates to a kit which comprises an oligonucleotide
CC detection assay configured for detecting the number of debrisoquine 4-
CC hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC identify the presence or absence of at least two CYP2D6 associated
CC polymorphisms. The kit and methods are useful for characterising
CC cytochrome p450 genes and alleles or for developing and optimising
CC nucleic acid detection assays for use in basic research, clinical
CC research and for the development of clinical detection assays. The
CC present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC target.
XX
SQ Sequence 44 BP; 7 A; 5 C; 27 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 36
AEC90075/c
ID AEC90075 standard; DNA; 44 BP.
XX
AC AEC90075;
XX
DT 17-NOV-2005 (first entry)
XX
DE CYP2D6 gene target region - SEQ ID 372.
XX
KW DNA detection; SNP detection; CYP2D6; ds.
XX
OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 4; SEQ ID NO 372; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a target region of the CYP2D6 gene which
CC was used in an example of the invention.
XX
SQ Sequence 44 BP; 7 A; 5 C; 27 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 37
AEC89995/c
ID   AEC89995 standard; DNA; 44 BP.
XX
AC   AEC89995;
XX
DT   17-NOV-2005  (first entry)
XX
DE   CYP2D6 gene target region - SEQ ID 292.
XX
KW   DNA detection; SNP detection; CYP2D6; ds.
XX
OS   Unidentified.
XX
PN   US2005196771-A1.
XX
PD   08-SEP-2005.
XX
PF   01-OCT-2004; 2004US-00956507.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
PR   10-JUL-2003; 2003US-00617070.
PR   02-OCT-2003; 2003US-0508220P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
PA   (CAOF/) CAO F.
PA   (OLDE/) OLDENBURG M C.
PA   (KOEL/) KOELBL J A.
PA   (AIZE/) AIZENSTEIN B D.
PA   (DAVE/) DAVEY K.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2005-637912/65.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies and for identifying the presence or absence
PT   of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT   having a CYP2D6 gene.
XX
PS   Example 3; SEQ ID NO 292; 189pp; English.
XX
CC   The invention comprises an oligonucleotide detection assay configured for
CC   detecting the number of CYP2D6 gene copies present in a sample, and
CC   configured for identifying the presence or absence of at least two CYP2D6
CC   -associated polymorphisms. The oligonucleotide detection assay of the
CC   invention is useful for genotyping a subject having a CYP2D6 gene. The
CC   present DNA sequence represents a target region of the CYP2D6 gene which
CC   was used in an example of the invention.
XX
SQ   Sequence 44 BP; 7 A; 5 C; 27 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 14;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 38
AEC89994/c
ID   AEC89994 standard; DNA; 44 BP.
XX
AC   AEC89994;
XX
DT   17-NOV-2005  (first entry)
XX
DE   CYP2D6 gene target region - SEQ ID 291.
XX
KW   DNA detection; SNP detection; CYP2D6; ds.
XX
OS   Unidentified.
XX
PN   US2005196771-A1.
XX
PD   08-SEP-2005.
XX
PF   01-OCT-2004; 2004US-00956507.
XX
PR   11-APR-2002; 2002US-0371819P.
PR   11-APR-2003; 2003US-00411954.
PR   10-JUL-2003; 2003US-00617070.
PR   02-OCT-2003; 2003US-0508220P.
XX
PA   (NEVI/) NEVILLE M.
PA   (INDI/) INDIG M D A.
PA   (CAOF/) CAO F.
PA   (OLDE/) OLDENBURG M C.
PA   (KOEL/) KOELBL J A.
PA   (AIZE/) AIZENSTEIN B D.
PA   (DAVE/) DAVEY K.
XX
PI   Neville M,  Indig MDA,  Cao F,  Oldenburg MC,  Koelbl JA;
PI   Aizenstein BD,  Davey K;
XX
DR   WPI; 2005-637912/65.
XX
PT   New kit comprising an oligonucleotide detection assay for detecting the
PT   number of CYP2D6 gene copies and for identifying the presence or absence
PT   of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT   having a CYP2D6 gene.
XX
PS   Example 3; SEQ ID NO 291; 189pp; English.
XX
CC   The invention comprises an oligonucleotide detection assay configured for
CC   detecting the number of CYP2D6 gene copies present in a sample, and
CC   configured for identifying the presence or absence of at least two CYP2D6
CC   -associated polymorphisms. The oligonucleotide detection assay of the
CC   invention is useful for genotyping a subject having a CYP2D6 gene. The
CC   present DNA sequence represents a target region of the CYP2D6 gene which
CC   was used in an example of the invention.
XX
SQ   Sequence 44 BP; 7 A; 4 C; 27 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 14;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 39
AEC90074/c
ID   AEC90074 standard; DNA; 44 BP.
XX
AC   AEC90074;
XX
DT   17-NOV-2005  (first entry)
XX
DE   CYP2D6 gene target region - SEQ ID 371.
XX
KW   DNA detection; SNP detection; CYP2D6; ds.
XX
```

OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 4; SEQ ID NO 371; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a target region of the CYP2D6 gene which
CC was used in an example of the invention.
XX
SQ Sequence 44 BP; 7 A; 4 C; 27 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 40
AEC89773/c
ID AEC89773 standard; DNA; 44 BP.
XX
AC AEC89773;
XX
DT 17-NOV-2005 (first entry)
XX
DE CYP2D6 gene target region - SEQ ID 70.
XX
KW DNA detection; SNP detection; CYP2D6; ds.
XX
OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.
PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 3; SEQ ID NO 70; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a target region of the CYP2D6 gene which
CC was used in an example of the invention.
XX
SQ Sequence 44 BP; 7 A; 5 C; 27 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 41
AEC89772/c
ID AEC89772 standard; DNA; 44 BP.
XX
AC AEC89772;
XX
DT 17-NOV-2005 (first entry)
XX
DE CYP2D6 gene target region - SEQ ID 69.
XX
KW DNA detection; SNP detection; CYP2D6; ds.
XX
OS Unidentified.
XX
PN US2005196771-A1.
XX
PD 08-SEP-2005.
XX
PF 01-OCT-2004; 2004US-00956507.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
PR 10-JUL-2003; 2003US-00617070.
PR 02-OCT-2003; 2003US-0508220P.
XX
PA (NEVI/) NEVILLE M.
PA (INDI/) INDIG M D A.
PA (CAOF/) CAO F.
PA (OLDE/) OLDENBURG M C.
PA (KOEL/) KOELBL J A.

PA (AIZE/) AIZENSTEIN B D.
PA (DAVE/) DAVEY K.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2005-637912/65.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies and for identifying the presence or absence
PT of CYP2D6 associated polymorphisms, useful for genotyping a subject
PT having a CYP2D6 gene.
XX
PS Example 3; SEQ ID NO 69; 189pp; English.
XX
CC The invention comprises an oligonucleotide detection assay configured for
CC detecting the number of CYP2D6 gene copies present in a sample, and
CC configured for identifying the presence or absence of at least two CYP2D6
CC -associated polymorphisms. The oligonucleotide detection assay of the
CC invention is useful for genotyping a subject having a CYP2D6 gene. The
CC present DNA sequence represents a target region of the CYP2D6 gene which
CC was used in an example of the invention.
XX
SQ Sequence 44 BP; 7 A; 4 C; 27 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 42
ABK30187
ID ABK30187 standard; DNA; 51 BP.
XX
AC ABK30187;
XX
DT 23-APR-2002 (first entry)
XX
DE CYP2D6 gene polymorphism detection primer #26.
XX
KW Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200196604-A2.
XX
PD 20-DEC-2001.
XX
PF 11-JUN-2001; 2001WO-US018912.
XX
PR 12-JUN-2000; 2000US-0210988P.
XX
PA (GENI-) GENICON SCI CORP.
XX
PI Bee G, Kohne DE, Korb L, Peterson T, Yguerabide J;
XX
DR WPI; 2002-130745/17.
XX
PT Determining the presence of a CYP2D6 target sequence in a DNA sample
PT containing CYP2D6 nucleic acid, for detecting mutations or polymorphisms,
PT comprises detecting the scattered light from a particle bound to the
PT target sequence.
XX
PS Example 2; Fig 6; 66pp; English.
XX
CC The invention relates to a method of determining the presence or absence
CC of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC acid. Determining the presence or absence of a CYP2D6 target sequence in
CC a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC nucleic acid with a probe under stringent binding conditions, and
CC detecting the presence or absence of the target sequence bound with the
CC probe with a scattered light detectable particle, by observing light
CC scattered from the particle which indicates the presence of the target
CC sequence. The method is useful for determining the presence or absence of
CC particular single nucleotide polymorphisms or alleles in genomic nucleic
CC acid, especially in a pharmacogenetically relevant gene or genes in a DNA
CC sample, and to detect and measure one or more target sequences in a
CC sample. The method may also be used to detect specific mutations to
CC identify the phenotypic classification of an individual. ABK30162-
CC ABK30230 represent CYP2D6 target sequence-specific primers of the
CC invention
XX
SQ Sequence 51 BP; 7 A; 28 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 9 CGCATCTCCCACCCCCA 25

RESULT 43
ABK30188
ID ABK30188 standard; DNA; 51 BP.
XX
AC ABK30188;
XX
DT 23-APR-2002 (first entry)
XX
DE CYP2D6 gene polymorphism detection primer #27.
XX
KW Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200196604-A2.
XX
PD 20-DEC-2001.
XX
PF 11-JUN-2001; 2001WO-US018912.
XX
PR 12-JUN-2000; 2000US-0210988P.
XX
PA (GENI-) GENICON SCI CORP.
XX
PI Bee G, Kohne DE, Korb L, Peterson T, Yguerabide J;
XX
DR WPI; 2002-130745/17.
XX
PT Determining the presence of a CYP2D6 target sequence in a DNA sample
PT containing CYP2D6 nucleic acid, for detecting mutations or polymorphisms,
PT comprises detecting the scattered light from a particle bound to the
PT target sequence.
XX
PS Example 2; Fig 6; 66pp; English.
XX
CC The invention relates to a method of determining the presence or absence
CC of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC acid. Determining the presence or absence of a CYP2D6 target sequence in
CC a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC nucleic acid with a probe under stringent binding conditions, and
CC detecting the presence or absence of the target sequence bound with the
CC probe with a scattered light detectable particle, by observing light
CC scattered from the particle which indicates the presence of the target
CC sequence. The method is useful for determining the presence or absence of
CC particular single nucleotide polymorphisms or alleles in genomic nucleic
CC acid, especially in a pharmacogenetically relevant gene or genes in a DNA
CC sample, and to detect and measure one or more target sequences in a

```
CC   sample. The method may also be used to detect specific mutations to
CC   identify the phenotypic classification of an individual. ABK30162-
CC   ABK30230 represent CYP2D6 target sequence-specific primers of the
CC   invention
XX
SQ   Sequence 51 BP; 8 A; 28 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 17;  DB 6;  Length 51;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          9 CGCATCTCCCACCCCCA 25


RESULT 44
ABK30182
ID   ABK30182 standard; DNA; 51 BP.
XX
AC   ABK30182;
XX
DT   23-APR-2002  (first entry)
XX
DE   CYP2D6 gene polymorphism detection primer #21.
XX
KW   Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200196604-A2.
XX
PD   20-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US018912.
XX
PR   12-JUN-2000; 2000US-0210988P.
XX
PA   (GENI-) GENICON SCI CORP.
XX
PI   Bee G,  Kohne DE,  Korb L,  Peterson T,  Yguerabide J;
XX
DR   WPI; 2002-130745/17.
XX
PT   Determining the presence of a CYP2D6 target sequence in a DNA sample
PT   containing CYP2D6 nucleic acid, for detecting mutations or polymorphisms,
PT   comprises detecting the scattered light from a particle bound to the
PT   target sequence.
XX
PS   Example 2; Fig 6; 66pp; English.
XX
CC   The invention relates to a method of determining the presence or absence
CC   of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC   acid. Determining the presence or absence of a CYP2D6 target sequence in
CC   a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC   nucleic acid with a probe under stringent binding conditions, and
CC   detecting the presence or absence of the target sequence bound with the
CC   probe with a scattered light detectable particle, by observing light
CC   scattered from the particle which indicates the presence of the target
CC   sequence. The method is useful for determining the presence or absence of
CC   particular single nucleotide polymorphisms or alleles in genomic nucleic
CC   acid, especially in a pharmacogenetically relevant gene or genes in a DNA
CC   sample, and to detect and measure one or more target sequences in a
CC   sample. The method may also be used to detect specific mutations to
CC   identify the phenotypic classification of an individual. ABK30162-
CC   ABK30230 represent CYP2D6 target sequence-specific primers of the
CC   invention
XX
SQ   Sequence 51 BP; 8 A; 28 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 17;  DB 6;  Length 51;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          9 CGCATCTCCCACCCCCA 25


RESULT 45
ABK30181
ID   ABK30181 standard; DNA; 51 BP.
XX
AC   ABK30181;
XX
DT   23-APR-2002  (first entry)
XX
DE   CYP2D6 gene polymorphism detection primer #20.
XX
KW   Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200196604-A2.
XX
PD   20-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US018912.
XX
PR   12-JUN-2000; 2000US-0210988P.
XX
PA   (GENI-) GENICON SCI CORP.
XX
PI   Bee G,  Kohne DE,  Korb L,  Peterson T,  Yguerabide J;
XX
DR   WPI; 2002-130745/17.
XX
PT   Determining the presence of a CYP2D6 target sequence in a DNA sample
PT   containing CYP2D6 nucleic acid, for detecting mutations or polymorphisms,
PT   comprises detecting the scattered light from a particle bound to the
PT   target sequence.
XX
PS   Example 2; Fig 6; 66pp; English.
XX
CC   The invention relates to a method of determining the presence or absence
CC   of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC   acid. Determining the presence or absence of a CYP2D6 target sequence in
CC   a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC   nucleic acid with a probe under stringent binding conditions, and
CC   detecting the presence or absence of the target sequence bound with the
CC   probe with a scattered light detectable particle, by observing light
CC   scattered from the particle which indicates the presence of the target
CC   sequence. The method is useful for determining the presence or absence of
CC   particular single nucleotide polymorphisms or alleles in genomic nucleic
CC   acid, especially in a pharmacogenetically relevant gene or genes in a DNA
CC   sample, and to detect and measure one or more target sequences in a
CC   sample. The method may also be used to detect specific mutations to
CC   identify the phenotypic classification of an individual. ABK30162-
CC   ABK30230 represent CYP2D6 target sequence-specific primers of the
CC   invention
XX
SQ   Sequence 51 BP; 7 A; 28 C; 7 G; 9 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 17;  DB 6;  Length 51;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          9 CGCATCTCCCACCCCCA 25


RESULT 46
ACC74032/c
```

```
ID   ACC74032 standard; DNA; 121 BP.
XX
AC   ACC74032;
XX
DT   11-JUL-2003  (first entry)
XX
DE   Human CYP2D6 targeting oligo SEQ ID NO: 102.
XX
KW   Human; cultured cell; coisogenic; genotypically distinct; target locus;
KW   ABCB1 (MDR1); targeting oligonucleotide; CYP2D6; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003027264-A2.
XX
PD   03-APR-2003.
XX
PF   27-SEP-2002; 2002WO-US031180.
XX
PR   27-SEP-2001; 2001US-0325992P.
XX
PA   (UYDE ) UNIV DELAWARE.
XX
PI   Kmiec EB,  Rice MC;
XX
DR   WPI; 2003-371919/35.
XX
PT   Novel cultured cell collection comprising at least 5 genotypically
PT   distinct cells each of which is coisogenic with respect to other cells at
PT   target locus common among them, useful for identifying target locus
PT   genotypes.
XX
PS   Example 2; Page 96; 112pp; English.
XX
CC   The invention relates to a novel collection of cultured cells, comprising
CC   at least 5 genotypically distinct cells, where each of the at least 5
CC   genotypically distinct cells is coisogenic with respect to the others of
CC   the at least 5 genotypically distinct cells at a target locus common
CC   among them, and where each of the at least 5 genotypically distinct cells
CC   can be separately assayed. The collection of cells is useful for
CC   identifying genotypes of a target locus that alter a cellular phenotype.
CC   The collection is also useful for pharmacogenomic studies, and in studies
CC   of structure-activity relationships of existing, and of potential new,
CC   therapeutic agents permitting multiplex analysis of the effects of amino
CC   acid changes on ligand-receptor interactions. The sequences shown in
CC   ACC79391-ACC73974 represent human ABCB1 (MDR1) targeting oligos. The
CC   sequences shown in ACC73975-ACC74126 represent human CYP2D6 targeting
CC   oligos
XX
SQ   Sequence 121 BP; 18 A; 34 C; 48 G; 21 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 8;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         90 CGCATCTCCCACCCCCA 74


RESULT 47
ACC74031
ID   ACC74031 standard; DNA; 121 BP.
XX
AC   ACC74031;
XX
DT   11-JUL-2003  (first entry)
XX
DE   Human CYP2D6 targeting oligo SEQ ID NO: 101.
XX
KW   Human; cultured cell; coisogenic; genotypically distinct; target locus;
KW   ABCB1 (MDR1); targeting oligonucleotide; CYP2D6; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003027264-A2.
XX
PD   03-APR-2003.
XX
PF   27-SEP-2002; 2002WO-US031180.
XX
PR   27-SEP-2001; 2001US-0325992P.
XX
PA   (UYDE ) UNIV DELAWARE.
XX
PI   Kmiec EB,  Rice MC;
XX
DR   WPI; 2003-371919/35.
XX
PT   Novel cultured cell collection comprising at least 5 genotypically
PT   distinct cells each of which is coisogenic with respect to other cells at
PT   target locus common among them, useful for identifying target locus
PT   genotypes.
XX
PS   Example 2; Page 95; 112pp; English.
XX
CC   The invention relates to a novel collection of cultured cells, comprising
CC   at least 5 genotypically distinct cells, where each of the at least 5
CC   genotypically distinct cells is coisogenic with respect to the others of
CC   the at least 5 genotypically distinct cells at a target locus common
CC   among them, and where each of the at least 5 genotypically distinct cells
CC   can be separately assayed. The collection of cells is useful for
CC   identifying genotypes of a target locus that alter a cellular phenotype.
CC   The collection is also useful for pharmacogenomic studies, and in studies
CC   of structure-activity relationships of existing, and of potential new,
CC   therapeutic agents permitting multiplex analysis of the effects of amino
CC   acid changes on ligand-receptor interactions. The sequences shown in
CC   ACC79391-ACC73974 represent human ABCB1 (MDR1) targeting oligos. The
CC   sequences shown in ACC73975-ACC74126 represent human CYP2D6 targeting
CC   oligos
XX
SQ   Sequence 121 BP; 21 A; 48 C; 34 G; 18 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 8;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         32 CGCATCTCCCACCCCCA 48


RESULT 48
ADM99817
ID   ADM99817 standard; DNA; 201 BP.
XX
AC   ADM99817;
XX
DT   15-JUL-2004  (first entry)
XX
DE   CYP2D6 (cytochrome p450 2D6) SNP-targeted probe 3.
XX
KW   genomic profile; health screening; SNP; single nucleotide polymorphism;
KW   drug toxicity; absorption, distribution, metabolism and elimination;
KW   ADME; ss; probe; CYP2D6; cytochrome p450 2D6.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 101
FT                   /*tag=  a
FT                   /note= "Due to presence of SNP (single nucleotide
FT                   polymorphism) in target DNA"
XX
PN   WO2004033722-A2.
XX
```

PD 22-APR-2004.
XX
PF 23-SEP-2003; 2003WO-GB004051.
XX
PR 23-SEP-2002; 2002GB-00022042.
XX
PA (SCIO-) SCIONA LTD.
XX
PI Roberts GW, Grimaldi K;
XX
DR WPI; 2004-364874/34.
XX
PT Set of probes for detecting relevant variants in target genes relating to
PT adverse events, comprises nucleotide probes complementary to DNA and RNA
PT sequences of genes such as apolipoprotein E gene, or angiotensinogen
PT gene.
XX
PS Example 4; Page 46; 68pp; English.
XX
CC The invention relates to a novel set of probes for detecting relevant
CC variants such as nucleotide substitutions, small deletions, repeated
CC variations etc. in a target group of genes that relate to adverse events.
CC The probes of the invention may be useful in biological assays for
CC detection of the gene variants, for measurement of differential gene
CC expression levels and for assessing the genomic profile of a patient
CC which may, in turn, be useful for general health screening, occupational
CC health purposes, health care planning on a population basis and other
CC health care management utilisations. The current sequence is that of a
CC CYP2D6 (cytochrome p450 2D6) SNP (single nucleotide polymorphism)-
CC targeted probe of the invention which may be used to assess an
CC individual's risk of drug toxicity on the basis that variation in genes
CC affects the absorption, distribution, metabolism and elimination (ADME)
CC of therapeutic substances.
XX
SQ Sequence 201 BP; 39 A; 72 C; 61 G; 28 T; 0 U; 1 Other;

Query Match 100.0%; Score 17; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 84 CGCATCTCCCACCCCCA 100

RESULT 49
AEF35799
ID AEF35799 standard; DNA; 347 BP.
XX
AC AEF35799;
XX
DT 23-MAR-2006 (first entry)
XX
DE Human cytochrome P450 2D6 DNA CYP2D6*4 polymorphism.
XX
KW diagnosis; prophylaxis; hepatitis B infection; hepatitis C infection;
KW hepatitis D infection; drug-induced hepatotoxicity; liver tumor;
KW liver cirrhosis; fibrosis; autoimmune hepatitis;
KW primary biliary cirrhosis; primary sclerosing cholangitis;
KW hemochromatosis; Wilson's disease; alpha-1 antitrypsin deficiency;
KW celiac disease; amyloidosis; gastrointestinal disease;
KW metabolic disorder; inflammation; cardiant; antiinflammatory;
KW hepatotropic; virucide; gastrointestinal-gen.; cns-gen.; metabolic;
KW immunosuppressive; cytostatic; cytochrome P450 2D6; CYP2D6; ds; SNP;
KW single nucleotide polymorphism; chromosome-22.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation 100
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
XX

PN WO2006003654-A2.
XX
PD 12-JAN-2006.
XX
PF 30-JUN-2005; 2005WO-IL000700.
XX
PR 01-JUL-2004; 2004US-0584179P.
XX
PA (MEDI-) MEDICAL RES FUND TEL AVIV SOURASKY MED.
XX
PI Oren R;
XX
DR WPI; 2006-090428/09.
XX
PT Determining if an individual is predisposed to fast progression of liver
PT fibrosis comprises determining a presence or absence of at least one fast
PT progression liver fibrosis-associated genotype.
XX
PS Claim 3; SEQ ID NO 1; 105pp; English.
XX
CC The invention relates to a method of determining if an individual is
CC predisposed to fast progression of liver fibrosis or liver cirrhosis
CC comprising determining a presence or absence, in a homozygous or
CC heterozygous form, of at least one fast progression liver fibrosis-
CC associated genotype in the CYP2D6, CYP3A5, CYP2E1, or APO E locus or in
CC neighboring loci of the individual, where the neighboring loci is in
CC linkage disequilibrium with the locus, thus determining if the individual
CC is predisposed to fast progression of liver fibrosis; a kit to carry out
CC the method; a method of preventing fast progression of liver fibrosis in
CC an individual, by upregulating CYP2D6 expression and/or activity; and a
CC method of determining if a drug molecule is capable of inducing or
CC accelerating development of fast progression of liver fibrosis in an
CC individual. The individual is suffering from a hepatitis viral infection
CC caused by hepatitis B, C or D virus, a hepatotoxicity (alcohol- or drug-
CC induced), a liver cancer, a non-alcoholic fatty liver disease (NAFLD), an
CC autoimmune disease (autoimmune hepatitis (AIH), primary biliary cirrhosis
CC (PBC), or primary sclerosing cholangitis (PSC)), a metabolic liver
CC disease (Hemochromatosis, Wilson's disease, or alpha 1 anti trypsin), or
CC a disease with secondary involvement of the liver (celiac disease and/or
CC amyloidosis). The method and kit are useful for determining if an
CC individual is predisposed to fast progression of liver fibrosis. The
CC method and drug are useful for preventing liver cirrhosis and fast
CC progression of liver fibrosis. This sequence is human cytochrome P450 2D6
CC DNA located on chromosome 22q13.1, showing the CYP2D6*4 single nucleotide
CC polymorphism.
XX
SQ Sequence 347 BP; 66 A; 107 C; 123 G; 50 T; 0 U; 1 Other;

Query Match 100.0%; Score 17; DB 15; Length 347;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 83 CGCATCTCCCACCCCCA 99

RESULT 50
AAL40743
ID AAL40743 standard; DNA; 400 BP.
XX
AC AAL40743;
XX
DT 25-SEP-2002 (first entry)
XX
DE DNA sequence of amplifier containing CYP450-2D6-G1749C SNP.
XX
KW Variation site; analysing; point mutation; detecting pathogen; SNP;
KW single nucleotide polymorphisms; paternity dispute; prenatal testing;
KW forensic analysis; CYP450.2D6.G1749C; ds.
XX
OS Unidentified.
XX

PN WO200194546-A2.
XX
PD 13-DEC-2001.
XX
PF 31-MAY-2001; 2001WO-US017928.
XX
PR 02-JUN-2000; 2000US-00585768.
XX
PA (DNAS-) DNA SCI INC.
XX
PI Xu H;
XX
DR WPI; 2002-566444/60.
XX
PT Analyzing variant site in target polynucleotide comprises using mixture
PT comprising labeled and unlabeled forms of nucleotide to generate labeled
PT extension products that are characteristic of nucleotide at variant
PT sites.
XX
PS Example 1; Fig 7; 63pp; English.
XX
CC The invention relates to a method for analysing a variation site in a
CC target polynucleotide. The method comprises contacting the target
CC polynucleotide with multiple copies of a primer hybridising adjacent to,
CC but not including, the variation site in the presence of a mixture of
CC labelled and unlabelled forms of a nucleotide under conditions such that
CC a copy of the primer is extended by incorporation of a labelled
CC nucleotide complementary to a base occupying the variation site in the
CC target polynucleotide; detecting the labelled nucleotide incorporated
CC into the primer as an indication of the variation site base. The methods
CC are useful for analysing variant sites in nucleic acids of interest,
CC including point mutations and single nucleotide polymorphisms (SNP), and
CC for detecting pathogens, paternity disputes, prenatal testing and
CC forensic analysis. This polynucleotide sequence represents the DNA of an
CC amplifier containing the CYP450.2D6.G1749C SNP relating to the invention
XX
SQ Sequence 400 BP; 66 A; 127 C; 139 G; 64 T; 0 U; 4 Other;

Query Match 100.0%; Score 17; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 313 CGCATCTCCCACCCCCA 329

RESULT 51
ADM99816
ID ADM99816 standard; DNA; 402 BP.
XX
AC ADM99816;
XX
DT 15-JUL-2004 (first entry)
XX
DE CYP2D6 (cytochrome p450 2D6) SNP-targeted probe 2.
XX
KW genomic profile; health screening; SNP; single nucleotide polymorphism;
KW drug toxicity; absorption, distribution, metabolism and elimination;
KW ADME; ss; probe; CYP2D6; cytochrome p450 2D6.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_difference 101
FT /*tag= a
FT /note= "Optionally absent due to presence of SNP (single
FT nucleotide polymorphism) in target DNA"
FT misc_difference 302
FT /*tag= a
FT /note= "Due to presence of SNP (single nucleotide
FT polymorphism) in target DNA"
XX

PN WO2004033722-A2.
XX
PD 22-APR-2004.
XX
PF 23-SEP-2003; 2003WO-GB004051.
XX
PR 23-SEP-2002; 2002GB-00022042.
XX
PA (SCIO-) SCIONA LTD.
XX
PI Roberts GW, Grimaldi K;
XX
DR WPI; 2004-364874/34.
XX
PT Set of probes for detecting relevant variants in target genes relating to
PT adverse events, comprises nucleotide probes complementary to DNA and RNA
PT sequences of genes such as apolipoprotein E gene, or angiotensinogen
PT gene.
XX
PS Example 4; Page 46; 68pp; English.
XX
CC The invention relates to a novel set of probes for detecting relevant
CC variants such as nucleotide substitutions, small deletions, repeated
CC variations etc. in a target group of genes that relate to adverse events.
CC The probes of the invention may be useful in biological assays for
CC detection of the gene variants, for measurement of differential gene
CC expression levels and for assessing the genomic profile of a patient
CC which may, in turn, be useful for general health screening, occupational
CC health purposes, health care planning on a population basis and other
CC health care management utilisations. The current sequence is that of a
CC CYP2D6 (cytochrome p450 2D6) SNP (single nucleotide polymorphism)-
CC targeted probe of the invention which may be used to assess an
CC individual's risk of drug toxicity on the basis that variation in genes
CC affects the absorption, distribution, metabolism and elimination (ADME)
CC of therapeutic substances.
XX
SQ Sequence 402 BP; 74 A; 127 C; 135 G; 65 T; 0 U; 1 Other;

Query Match 100.0%; Score 17; DB 12; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 382 CGCATCTCCCACCCCCA 398

RESULT 52
ADO84826
ID ADO84826 standard; DNA; 483 BP.
XX
AC ADO84826;
XX
DT 29-JUL-2004 (first entry)
XX
DE CYP2 plasmid DNA #14.
XX
KW Single nucleotide polymorphism; SNP; CYP2; streptavidin; St;
KW horseradish peroxidase; pharmaceutical intolerance; ds.
XX
OS Synthetic.
XX
PN DE10237691-A1.
XX
PD 04-MAR-2004.
XX
PF 15-AUG-2002; 2002DE-01037691.
XX
PR 15-AUG-2002; 2002DE-01037691.
XX
PA (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.
XX
PI Neunaber R, Strohner P, Schreiber J, Voigt G, Schunck W;

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XX
DR   WPI; 2004-248950/24.
XX
PT   Detecting single-nucleotide polymorphisms in human CYP2 genes, useful for
PT   diagnosis of pharmaceutical intolerances, using specific primers or
PT   probes.
XX
PS   Disclosure; SEQ ID NO 50; 28pp; German.
XX
CC   The invention relates to a method of detecting single-nucleotide
CC   polymorphisms (SNPs) in human CYP2 genes using specified primers and/or
CC   probes. The method comprises detection of the CYP2 alleles in artificial
CC   plasmids. The primers are used in a hybridisation assay to detect alleles
CC   in genomic DNA, from both homozygous and heterozygous carriers. The assay
CC   comprises labelling one primer per gene segment with biotin, amplifying
CC   the allele-defining gene segments by PCR, binding the labelled amplicon
CC   to heat-stable streptavidin (St)-coated plates, removing the
CC   contaminating genomic DNA and the complementary strands by stringent
CC   washing, hybridising the bound single-stranded amplicon to an allele-
CC   specific FITC (fluorescein isothiocyanate)-labelled oligonucleotide,
CC   removing the unbound oligonucleotide by washing, and detecting the allele
CC   -presented oligonucleotide by ELISA using an antibody against FITC that
CC   is conjugated to horseradish peroxidase. The method is useful for
CC   detecting SNPs in CYP2 genes that are associated with an absence, or
CC   reduction, of enzymatic activity, particularly for diagnosis of
CC   intolerances of pharmaceuticals. This sequence represents CYP2 plasmid
CC   DNA used in the method of the invention.
XX
SQ   Sequence 483 BP; 81 A; 159 C; 166 G; 77 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 483;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        265 CGCATCTCCCACCCCCA 281


RESULT 53
AEC32560
ID   AEC32560 standard; DNA; 483 BP.
XX
AC   AEC32560;
XX
DT   03-NOV-2005  (first entry)
XX
DE   Plasmid CYP2D6*6 mutant DNA fragment.
XX
KW   ds; detection; single nucleotide polymorphism; SNP; CYP2;
KW   cytochrome P450 2; diagnostic; cytochrome P450;
KW   isoform-specific polymer chain reaction; IS-PCR; plasmid; circular.
XX
OS   Synthetic.
XX
PN   DE102004006477-A1.
XX
PD   25-AUG-2005.
XX
PF   04-FEB-2004; 2004DE-10006477.
XX
PR   04-FEB-2004; 2004DE-10006477.
XX
PA   (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.
XX
PI   Neunaber R,  Strohner P,  Schreiber J,  Voigt G;
XX
DR   WPI; 2005-592623/61.
XX
PT   Process for demonstrating the presence of single nucleotide polymorphism
PT   in human genes, comprises using a priming agent.
XX
PS   Claim 1; SEQ ID NO 50; 77pp; German.
XX
CC   This invention describes a novel method of detecting the presence of
CC   single nucleotide polymorphisms (SNPs) in human CYP2-genes using a
CC   priming agent and/or a probe, where the priming agent effects high-
CC   resolution amplification of the respective CYP2 allelomorph. The method
CC   can be incorporated into a diagnostic kit that detects the presence of
CC   polymorphisms in human cytochrome P450 genes comprising a synthetic
CC   oligonucleotide that amplifies isoform-specific (IS-PCR) polymer chain
CC   reactions using a DNA polymerase chain reaction. The kit components
CC   selectively immobilize single-stranded biotinized IS-PCR products on
CC   streptavidin-coated micro-titration slides under stable thermal
CC   conditions. Test-optimized, allelmorph-specific, fluorescein
CC   isothiocyanate (FITC)-marked synthetic oligonucleotides facilitate
CC   accurate identification of the genotype of the immobilized amplification
CC   products through a sequence of hybridization, subsequent washing and
CC   detection by fluorometry or photometry. The novel diagnostic process is
CC   rapid and cost-effective. This sequence represents a plasmid fragment
CC   used in the detection method of the invention.
XX
SQ   Sequence 483 BP; 81 A; 159 C; 166 G; 77 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 14;  Length 483;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        265 CGCATCTCCCACCCCCA 281


RESULT 54
ADO84825
ID   ADO84825 standard; DNA; 484 BP.
XX
AC   ADO84825;
XX
DT   29-JUL-2004  (first entry)
XX
DE   CYP2 plasmid DNA #13.
XX
KW   Single nucleotide polymorphism; SNP; CYP2; streptavidin; St;
KW   horseradish peroxidase; pharmaceutical intolerance; ds.
XX
OS   Synthetic.
XX
PN   DE10237691-A1.
XX
PD   04-MAR-2004.
XX
PF   15-AUG-2002; 2002DE-01037691.
XX
PR   15-AUG-2002; 2002DE-01037691.
XX
PA   (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.
XX
PI   Neunaber R,  Strohner P,  Schreiber J,  Voigt G,  Schunck W;
XX
DR   WPI; 2004-248950/24.
XX
PT   Detecting single-nucleotide polymorphisms in human CYP2 genes, useful for
PT   diagnosis of pharmaceutical intolerances, using specific primers or
PT   probes.
XX
PS   Disclosure; SEQ ID NO 49; 28pp; German.
XX
CC   The invention relates to a method of detecting single-nucleotide
CC   polymorphisms (SNPs) in human CYP2 genes using specified primers and/or
CC   probes. The method comprises detection of the CYP2 alleles in artificial
CC   plasmids. The primers are used in a hybridisation assay to detect alleles
CC   in genomic DNA, from both homozygous and heterozygous carriers. The assay
CC   comprises labelling one primer per gene segment with biotin, amplifying
CC   the allele-defining gene segments by PCR, binding the labelled amplicon
CC   to heat-stable streptavidin (St)-coated plates, removing the
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```
CC   contaminating genomic DNA and the complementary strands by stringent
CC   washing, hybridising the bound single-stranded amplicon to an allele-
CC   specific FITC (fluorescein isothiocyanate)-labelled oligonucleotide,
CC   removing the unbound oligonucleotide by washing, and detecting the allele
CC   -presented oligonucleotide by ELISA using an antibody against FITC that
CC   is conjugated to horseradish peroxidase. The method is useful for
CC   detecting SNPs in CYP2 genes that are associated with an absence, or
CC   reduction, of enzymatic activity, particularly for diagnosis of
CC   intolerances of pharmaceuticals. This sequence represents CYP2 plasmid
CC   DNA used in the method of the invention.
XX
SQ   Sequence 484 BP; 81 A; 159 C; 166 G; 78 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 17;  DB 12;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        266 CGCATCTCCCACCCCCA 282


RESULT 55
AEC32559
ID   AEC32559 standard; DNA; 484 BP.
XX
AC   AEC32559;
XX
DT   03-NOV-2005  (first entry)
XX
DE   Plasmid CYP2D6*6 wild type DNA fragment.
XX
KW   ds; detection; single nucleotide polymorphism; SNP; CYP2;
KW   cytochrome P450 2; diagnostic; cytochrome P450;
KW   isoform-specific polymer chain reaction; IS-PCR; plasmid; circular.
XX
OS   Synthetic.
XX
PN   DE102004006477-A1.
XX
PD   25-AUG-2005.
XX
PF   04-FEB-2004; 2004DE-10006477.
XX
PR   04-FEB-2004; 2004DE-10006477.
XX
PA   (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.
XX
PI   Neunaber R,  Strohner P,  Schreiber J,  Voigt G;
XX
DR   WPI; 2005-592623/61.
XX
PT   Process for demonstrating the presence of single nucleotide polymorphism
PT   in human genes, comprises using a priming agent.
XX
PS   Claim 1; SEQ ID NO 49; 77pp; German.
XX
CC   This invention describes a novel method of detecting the presence of
CC   single nucleotide polymorphisms (SNPs) in human CYP2-genes using a
CC   priming agent and/or a probe, where the priming agent effects high-
CC   resolution amplification of the respective CYP2 allelomorph. The method
CC   can be incorporated into a diagnostic kit that detects the presence of
CC   polymorphisms in human cytochrome P450 genes comprising a synthetic
CC   oligonucleotide that amplifies isoform-specific (IS-PCR) polymer chain
CC   reactions using a DNA polymerase chain reaction. The kit components
CC   selectively immobilize single-stranded biotinized IS-PCR products on
CC   streptavidin-coated micro-titration slides under stable thermal
CC   conditions. Test-optimized, allelmorph-specific, fluorescein
CC   isothiocyanate (FITC)-marked synthetic oligonucleotides facilitate
CC   accurate identification of the genotype of the immobilized amplification
CC   products through a sequence of hybridization, subsequent washing and
CC   detection by fluorometry or photometry. The novel diagnostic process is
CC   rapid and cost-effective. This sequence represents a plasmid fragment
CC   used in the detection method of the invention.
XX
SQ   Sequence 484 BP; 81 A; 159 C; 166 G; 78 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 17;  DB 14;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        266 CGCATCTCCCACCCCCA 282


RESULT 56
ABT33980
ID   ABT33980 standard; DNA; 490 BP.
XX
AC   ABT33980;
XX
DT   29-MAY-2003  (first entry)
XX
DE   Human pigmentation trait-related DNA - SEQ ID No 79.
XX
KW   Human; single nucleotide polymorphism; SNP; ds; melanocortin-1 receptor;
KW   genetic pigmentation trait; MC1R; agouti signaling protein; ASIP; race;
KW   hair colour; eye colour; forensic tool.
XX
OS   Homo sapiens.
XX
PN   WO200297047-A2.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016789.
XX
PR   25-MAY-2001; 2001US-0293560P.
PR   21-JUN-2001; 2001US-0300187P.
PR   07-AUG-2001; 2001US-0310781P.
PR   17-SEP-2001; 2001US-0323662P.
PR   26-OCT-2001; 2001US-0344418P.
PR   15-NOV-2001; 2001US-0334674P.
PR   02-JAN-2002; 2002US-0346303P.
XX
PA   (DNAP-) DNAPRINT GENOMICS INC.
XX
PI   Frudakis T;
XX
DR   WPI; 2003-239091/23.
XX
PT   Inferring genetic pigmentation trait such as hair/eye color or shade from
PT   nucleic acid sample of human subject, by identifying a pigmentation-
PT   related haplotype allele of a pigmentation gene in the sample.
XX
PS   Claim 50; Page 362; 396pp; English.
XX
CC   The invention comprises a method for inferring a genetic pigmentation
CC   trait of a human. The method involves identifying a single nucleotide
CC   polymorphism (SNP) in a pigmentation gene - where the pigmentation gene
CC   is not melanocortin-1 receptor (MC1R) and agouti signaling protein
CC   (ASIP). The method of the invention is useful for inferring a genetic
CC   pigmentation trait of a human, especially for inferring the race of a
CC   human subject. The method is useful for inferring a genetic pigmentation
CC   trait such as hair shade or colour, or eye shade or colour of a human
CC   subject. The method may be used as a forensic tool for obtaining
CC   information relating to physical characteristics of a potential crime
CC   victim or a perpetrator of a crime from a nucleic acid sample present at
CC   a crime scene. The present human DNA sequence is used in the
CC   exemplification of the invention
XX
SQ   Sequence 490 BP; 92 A; 139 C; 182 G; 71 T; 0 U; 6 Other;

  Query Match            100.0%;  Score 17;  DB 8;  Length 490;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
```

```
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        438 CGCATCTCCCACCCCCA 454


RESULT 57
ADC26791
ID   ADC26791 standard; DNA; 490 BP.
XX
AC   ADC26791;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human lipitor/zocor response-related SNP DNA - SEQ ID 201.
XX
KW   statin response; cytochrome p450 3A4; CYP3A4; 2D6; CYP2D6;
KW   3-hydroxy-3-methylglutaryl-coenzyme A reductase; HMGCR; atorvastatin;
KW   simvastatin; serum cholesterol level; heart attack;
KW   single nucleotide polymorphism; SNP; human; ds; lipitor; zocor.
XX
OS   Homo sapiens.
XX
PN   WO2003002721-A2.
XX
PD   09-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020847.
XX
PR   29-JUN-2001; 2001US-0301867P.
PR   07-AUG-2001; 2001US-0310783P.
PR   13-SEP-2001; 2001US-0322478P.
XX
PA   (DNAP-) DNAPRINT GENOMICS INC.
XX
PI   Frudakis T;
XX
DR   WPI; 2003-239174/23.
XX
PT   Inferring a statin response from a nucleic acid sample, by haplotype
PT   allele indicative of statin response, a decrease in total cholesterol, or
PT   in low density lipoprotein infers a statin response of the subject.
XX
PS   Example 9; SEQ ID NO 201; 323pp; English.
XX
CC   The invention relates to a novel method for inferring a statin response
CC   from a nucleic acid sample comprising identifying in the nucleic acid
CC   sample, at least one haplotype allele indicative of a statin response.
CC   The haplotype allele may comprise nucleotides of the cytochrome p450 3A4
CC   (CYP3A4) gene, nucleotides of the cytochrome p450 2D6 (CYP2D6) gene or
CC   nucleotides of the 3-hydroxy-3-methylglutaryl-coenzyme A reductase
CC   (HMGCR) gene. The method of the invention may be useful for inferring a
CC   statin response of a human subject from a nucleic acid sample, where the
CC   human subject is a Caucasian subject and the statin is atorvastatin or
CC   simvastatin. The method may also be useful for determining whether to
CC   prescribe statin to a patient with elevated serum cholesterol levels in
CC   order to prevent heart attack. The current sequence is that of the human
CC   lipitor/zocor response-related SNP DNA of the invention.
XX
SQ   Sequence 490 BP; 92 A; 139 C; 182 G; 71 T; 0 U; 6 Other;

  Query Match             100.0%;  Score 17;  DB 10;  Length 490;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        438 CGCATCTCCCACCCCCA 454


RESULT 58
AEE02739
ID   AEE02739 standard; cDNA; 500 BP.
XX
AC   AEE02739;
XX
DT   09-FEB-2006  (first entry)
XX
DE   Human Cytochrome P450 2D6 cDNA SEQ ID NO: 1.
XX
KW   ss; coding sequence; drug metabolism; cytochrome P450 2D6; CYP 2D6; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(246,A)
FT                   /*tag=  a
FT                   /standard_name= "Single nulceotide polymorphism"
FT                   /note= "This variant is shown in SEQ ID NO: 2"
XX
PN   JP2005328712-A.
XX
PD   02-DEC-2005.
XX
PF   18-MAY-2004; 2004JP-00147651.
XX
PR   18-MAY-2004; 2004JP-00147651.
XX
PA   (KYOT-) KYOTO DAIICHI KAGAKU KK.
XX
PI   Hirai M;
XX
DR   WPI; 2006-013653/02.
XX
PT   Novel nucleic acid probe labeled by fluorescent dye at 3' terminal,
PT   useful for detecting single nucleotide polymorphism G1846A in cDNA of
PT   CYP2D6 gene.
XX
PS   Claim 1; SEQ ID NO 1; 12pp; Japanese.
XX
CC   The present sequence is that cDNA corresponding to one allelic variant of
CC   the human cytochrome P450 2D6. The present invention relates to a method
CC   of detecting a G1846A single nucleotide polymorphism (SNP) in the gene
CC   sequence of human cytochrome P450 2D6 which metabolizes various
CC   clinically important drug compounds including beta-blockers,
CC   antiarrhythmic drugs and antihistamine drugs. This SNP causes a less
CC   rapid metabolism of such drugs and increases the risks (e.g. side
CC   effects) associated with them. The method of the invention involves
CC   amplifying the region containing the G1846A polymorphism by PCR, binding
CC   a fluorescently labeled nucleic acid probe targeted to this region and
CC   producing a melting temperature curve by measuring the fluorescent signal
CC   at differing temperatures. This melting temperature curve is then
CC   analyzed and the variant present is determined.
XX
SQ   Sequence 500 BP; 84 A; 155 C; 181 G; 80 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 15;  Length 500;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        229 CGCATCTCCCACCCCCA 245


RESULT 59
AEE02740
ID   AEE02740 standard; cDNA; 500 BP.
XX
AC   AEE02740;
XX
DT   09-FEB-2006  (first entry)
XX
DE   Human Cytochrome P450 2D6 cDNA SEQ ID NO: 2.
```

XX
KW ss; coding sequence; drug metabolism; cytochrome P450 2D6; CYP 2D6; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(246,G)
FT /*tag= a
FT /standard_name= "Single nulceotide polymorphism"
FT /note= "This variant is shown in SEQ ID NO: 1"
XX
PN JP2005328712-A.
XX
PD 02-DEC-2005.
XX
PF 18-MAY-2004; 2004JP-00147651.
XX
PR 18-MAY-2004; 2004JP-00147651.
XX
PA (KYOT-) KYOTO DAIICHI KAGAKU KK.
XX
PI Hirai M;
XX
DR WPI; 2006-013653/02.
XX
PT Novel nucleic acid probe labeled by fluorescent dye at 3' terminal,
PT useful for detecting single nucleotide polymorphism G1846A in cDNA of
PT CYP2D6 gene.
XX
PS Claim 1; SEQ ID NO 2; 12pp; Japanese.
XX
CC The present sequence is that cDNA corresponding to one allelic variant of
CC the human cytochrome P450 2D6. The present invention relates to a method
CC of detecting a G1846A single nucleotide polymorphism (SNP) in the gene
CC sequence of human cytochrome P450 2D6 which metabolizes various
CC clinically important drug compounds including beta-blockers,
CC antiarrhythmic drugs and antihistamine drugs. This SNP causes a less
CC rapid metabolism of such drugs and increases the risks (e.g. side
CC effects) associated with them. The method of the invention involves
CC amplifying the region containing the G1846A polymorphism by PCR, binding
CC a fluorescently labeled nucleic acid probe targeted to this region and
CC producing a melting temperature curve by measuring the fluorescent signal
CC at differing temperatures. This melting temperature curve is then
CC analyzed and the variant present is determined.
XX
SQ Sequence 500 BP; 85 A; 155 C; 180 G; 80 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 15; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 229 CGCATCTCCCACCCCCA 245

RESULT 60
ADO84823
ID ADO84823 standard; DNA; 652 BP.
XX
AC ADO84823;
XX
DT 29-JUL-2004 (first entry)
XX
DE CYP2 plasmid DNA #11.
XX
KW Single nucleotide polymorphism; SNP; CYP2; streptavidin; St;
KW horseradish peroxidase; pharmaceutical intolerance; ds.
XX
OS Synthetic.
XX
PN DE10237691-A1.
XX
PD 04-MAR-2004.
XX
PF 15-AUG-2002; 2002DE-01037691.
XX
PR 15-AUG-2002; 2002DE-01037691.
XX
PA (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.
XX
PI Neunaber R, Strohner P, Schreiber J, Voigt G, Schunck W;
XX
DR WPI; 2004-248950/24.
XX
PT Detecting single-nucleotide polymorphisms in human CYP2 genes, useful for
PT diagnosis of pharmaceutical intolerances, using specific primers or
PT probes.
XX
PS Disclosure; SEQ ID NO 47; 28pp; German.
XX
CC The invention relates to a method of detecting single-nucleotide
CC polymorphisms (SNPs) in human CYP2 genes using specified primers and/or
CC probes. The method comprises detection of the CYP2 alleles in artificial
CC plasmids. The primers are used in a hybridisation assay to detect alleles
CC in genomic DNA, from both homozygous and heterozygous carriers. The assay
CC comprises labelling one primer per gene segment with biotin, amplifying
CC the allele-defining gene segments by PCR, binding the labelled amplicon
CC to heat-stable streptavidin (St)-coated plates, removing the
CC contaminating genomic DNA and the complementary strands by stringent
CC washing, hybridising the bound single-stranded amplicon to an allele-
CC specific FITC (fluorescein isothiocyanate)-labelled oligonucleotide,
CC removing the unbound oligonucleotide by washing, and detecting the allele
CC -presented oligonucleotide by ELISA using an antibody against FITC that
CC is conjugated to horseradish peroxidase. The method is useful for
CC detecting SNPs in CYP2 genes that are associated with an absence, or
CC reduction, of enzymatic activity, particularly for diagnosis of
CC intolerances of pharmaceuticals. This sequence represents CYP2 plasmid
CC DNA used in the method of the invention.
XX
SQ Sequence 652 BP; 116 A; 187 C; 240 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 652;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 298 CGCATCTCCCACCCCCA 314

RESULT 61
ADO84824
ID ADO84824 standard; DNA; 652 BP.
XX
AC ADO84824;
XX
DT 29-JUL-2004 (first entry)
XX
DE CYP2 plasmid DNA #12.
XX
KW Single nucleotide polymorphism; SNP; CYP2; streptavidin; St;
KW horseradish peroxidase; pharmaceutical intolerance; ds.
XX
OS Synthetic.
XX
PN DE10237691-A1.
XX
PD 04-MAR-2004.
XX
PF 15-AUG-2002; 2002DE-01037691.
XX
PR 15-AUG-2002; 2002DE-01037691.
XX
PA (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.

XX
PI Neunaber R, Strohner P, Schreiber J, Voigt G, Schunck W;
XX
DR WPI; 2004-248950/24.
XX
PT Detecting single-nucleotide polymorphisms in human CYP2 genes, useful for
PT diagnosis of pharmaceutical intolerances, using specific primers or
PT probes.
XX
PS Disclosure; SEQ ID NO 48; 28pp; German.
XX
CC The invention relates to a method of detecting single-nucleotide
CC polymorphisms (SNPs) in human CYP2 genes using specified primers and/or
CC probes. The method comprises detection of the CYP2 alleles in artificial
CC plasmids. The primers are used in a hybridisation assay to detect alleles
CC in genomic DNA, from both homozygous and heterozygous carriers. The assay
CC comprises labelling one primer per gene segment with biotin, amplifying
CC the allele-defining gene segments by PCR, binding the labelled amplicon
CC to heat-stable streptavidin (St)-coated plates, removing the
CC contaminating genomic DNA and the complementary strands by stringent
CC washing, hybridising the bound single-stranded amplicon to an allele-
CC specific FITC (fluorescein isothiocyanate)-labelled oligonucleotide,
CC removing the unbound oligonucleotide by washing, and detecting the allele
CC -presented oligonucleotide by ELISA using an antibody against FITC that
CC is conjugated to horseradish peroxidase. The method is useful for
CC detecting SNPs in CYP2 genes that are associated with an absence, or
CC reduction, of enzymatic activity, particularly for diagnosis of
CC intolerances of pharmaceuticals. This sequence represents CYP2 plasmid
CC DNA used in the method of the invention.
XX
SQ Sequence 652 BP; 117 A; 187 C; 239 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 652;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 298 CGCATCTCCCACCCCCA 314

RESULT 62
AEC32557
ID AEC32557 standard; DNA; 652 BP.
XX
AC AEC32557;
XX
DT 03-NOV-2005 (first entry)
XX
DE Plasmid CYP2D6*4 wild type DNA fragment.
XX
KW ds; detection; single nucleotide polymorphism; SNP; CYP2;
KW cytochrome P450 2; diagnostic; cytochrome P450;
KW isoform-specific polymer chain reaction; IS-PCR; plasmid; circular.
XX
OS Synthetic.
XX
PN DE102004006477-A1.
XX
PD 25-AUG-2005.
XX
PF 04-FEB-2004; 2004DE-10006477.
XX
PR 04-FEB-2004; 2004DE-10006477.
XX
PA (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.
XX
PI Neunaber R, Strohner P, Schreiber J, Voigt G;
XX
DR WPI; 2005-592623/61.
XX
PT Process for demonstrating the presence of single nucleotide polymorphism
PT in human genes, comprises using a priming agent.
XX
PS Claim 1; SEQ ID NO 47; 77pp; German.
XX
CC This invention describes a novel method of detecting the presence of
CC single nucleotide polymorphisms (SNPs) in human CYP2-genes using a
CC priming agent and/or a probe, where the priming agent effects high-
CC resolution amplification of the respective CYP2 allelomorph. The method
CC can be incorporated into a diagnostic kit that detects the presence of
CC polymorphisms in human cytochrome P450 genes comprising a synthetic
CC oligonucleotide that amplifies isoform-specific (IS-PCR) polymer chain
CC reactions using a DNA polymerase chain reaction. The kit components
CC selectively immobilize single-stranded biotinized IS-PCR products on
CC streptavidin-coated micro-titration slides under stable thermal
CC conditions. Test-optimized, allelmorph-specific, fluorescein
CC isothiocyanate (FITC)-marked synthetic oligonucleotides facilitate
CC accurate identification of the genotype of the immobilized amplification
CC products through a sequence of hybridization, subsequent washing and
CC detection by fluorometry or photometry. The novel diagnostic process is
CC rapid and cost-effective. This sequence represents a plasmid fragment
CC used in the detection method of the invention.
XX
SQ Sequence 652 BP; 116 A; 187 C; 240 G; 109 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 652;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 298 CGCATCTCCCACCCCCA 314

RESULT 63
AEC32558
ID AEC32558 standard; DNA; 652 BP.
XX
AC AEC32558;
XX
DT 03-NOV-2005 (first entry)
XX
DE Plasmid CYP2D6*4 mutant DNA fragment.
XX
KW ds; detection; single nucleotide polymorphism; SNP; CYP2;
KW cytochrome P450 2; diagnostic; cytochrome P450;
KW isoform-specific polymer chain reaction; IS-PCR; plasmid; circular.
XX
OS Synthetic.
XX
PN DE102004006477-A1.
XX
PD 25-AUG-2005.
XX
PF 04-FEB-2004; 2004DE-10006477.
XX
PR 04-FEB-2004; 2004DE-10006477.
XX
PA (BIOT-) BIOTEZ BERLIN-BUCH GMBH BIOCHEMISCH.
XX
PI Neunaber R, Strohner P, Schreiber J, Voigt G;
XX
DR WPI; 2005-592623/61.
XX
PT Process for demonstrating the presence of single nucleotide polymorphism
PT in human genes, comprises using a priming agent.
XX
PS Claim 1; SEQ ID NO 48; 77pp; German.
XX
CC This invention describes a novel method of detecting the presence of
CC single nucleotide polymorphisms (SNPs) in human CYP2-genes using a
CC priming agent and/or a probe, where the priming agent effects high-
CC resolution amplification of the respective CYP2 allelomorph. The method
CC can be incorporated into a diagnostic kit that detects the presence of
CC polymorphisms in human cytochrome P450 genes comprising a synthetic

```
CC   oligonucleotide that amplifies isoform-specific (IS-PCR) polymer chain
CC   reactions using a DNA polymerase chain reaction. The kit components
CC   selectively immobilize single-stranded biotinized IS-PCR products on
CC   streptavidin-coated micro-titration slides under stable thermal
CC   conditions. Test-optimized, allelmorph-specific, fluorescein
CC   isothiocyanate (FITC)-marked synthetic oligonucleotides facilitate
CC   accurate identification of the genotype of the immobilized amplification
CC   products through a sequence of hybridization, subsequent washing and
CC   detection by fluorometry or photometry. The novel diagnostic process is
CC   rapid and cost-effective. This sequence represents a plasmid fragment
CC   used in the detection method of the invention.
XX
SQ   Sequence 652 BP; 117 A; 187 C; 239 G; 109 T; 0 U; 0 Other;

  Query Match          100.0%;  Score 17;  DB 14;  Length 652;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        298 CGCATCTCCCACCCCCA 314


RESULT 64
ADM94996
ID   ADM94996 standard; DNA; 901 BP.
XX
AC   ADM94996;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human cytochrome P450 2D6 (CYP2D*6) gene.
XX
KW   Single-nucleotide polymorphism; SNP; polymorphism detection; human;
KW   cytochrome P450 2D6; CYP2D6; ds.
XX
OS   Homo sapiens.
XX
PN   US2003175728-A1.
XX
PD   18-SEP-2003.
XX
PF   06-JUN-2002; 2002US-00165410.
XX
PR   08-DEC-1999;   99US-00457616.
PR   06-JUN-2001; 2001US-00876830.
PR   29-JUN-2001; 2001US-0302137P.
PR   23-JAN-2002; 2002US-0351637P.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Belousov YS,  Afonina IA;
XX
DR   WPI; 2004-009711/01.
XX
PT   Continuous monitoring of nucleic acid amplification, useful e.g. for
PT   detecting polymorphisms, using modified fluorescent probe that binds
PT   specifically to amplicon.
XX
PS   Example 1; Page 24; 43pp; English.
XX
CC   The invention relates to a method for continuous monitoring of
CC   polynucleotide amplification from the hybridisation of a labelled
CC   oligonucleotide conjugate to the amplified target. The labelled
CC   oligonucleotides are used for (real-time) monitoring of amplification and
CC   gene expression; to detect single-nucleotide polymorphisms; to detect a
CC   target in a mixture with related sequences; and to distinguish between
CC   wild-type, mutant and heterozygous target polynucleotides. The present
CC   sequence is human cytochrome P450 2D6 (CYP2D6) gene. This sequence is
CC   used to illustrate the method of the invention.
XX
SQ   Sequence 901 BP; 172 A; 247 C; 334 G; 148 T; 0 U; 0 Other;

  Query Match          100.0%;  Score 17;  DB 12;  Length 901;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        448 CGCATCTCCCACCCCCA 464


RESULT 65
ABT33976
ID   ABT33976 standard; DNA; 1190 BP.
XX
AC   ABT33976;
XX
DT   29-MAY-2003  (first entry)
XX
DE   Human pigmentation trait-related DNA - SEQ ID No 75.
XX
KW   Human; single nucleotide polymorphism; SNP; ds; melanocortin-1 receptor;
KW   genetic pigmentation trait; MC1R; agouti signaling protein; ASIP; race;
KW   hair colour; eye colour; forensic tool.
XX
OS   Homo sapiens.
XX
PN   WO200297047-A2.
XX
PD   05-DEC-2002.
XX
PF   28-MAY-2002; 2002WO-US016789.
XX
PR   25-MAY-2001; 2001US-0293560P.
PR   21-JUN-2001; 2001US-0300187P.
PR   07-AUG-2001; 2001US-0310781P.
PR   17-SEP-2001; 2001US-0323662P.
PR   26-OCT-2001; 2001US-0344418P.
PR   15-NOV-2001; 2001US-0334674P.
PR   02-JAN-2002; 2002US-0346303P.
XX
PA   (DNAP-) DNAPRINT GENOMICS INC.
XX
PI   Frudakis T;
XX
DR   WPI; 2003-239091/23.
XX
PT   Inferring genetic pigmentation trait such as hair/eye color or shade from
PT   nucleic acid sample of human subject, by identifying a pigmentation-
PT   related haplotype allele of a pigmentation gene in the sample.
XX
PS   Claim 50; Page 359-360; 396pp; English.
XX
CC   The invention comprises a method for inferring a genetic pigmentation
CC   trait of a human. The method involves identifying a single nucleotide
CC   polymorphism (SNP) in a pigmentation gene - where the pigmentation gene
CC   is not melanocortin-1 receptor (MC1R) and agouti signaling protein
CC   (ASIP). The method of the invention is useful for inferring a genetic
CC   pigmentation trait of a human, especially for inferring the race of a
CC   human subject. The method is useful for inferring a genetic pigmentation
CC   trait such as hair shade or colour, or eye shade or colour of a human
CC   subject. The method may be used as a forensic tool for obtaining
CC   information relating to physical characteristics of a potential crime
CC   victim or a perpetrator of a crime from a nucleic acid sample present at
CC   a crime scene. The present human DNA sequence is used in the
CC   exemplification of the invention
XX
SQ   Sequence 1190 BP; 230 A; 323 C; 433 G; 202 T; 0 U; 2 Other;

  Query Match          100.0%;  Score 17;  DB 8;  Length 1190;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
```

```
Db        438 CGCATCTCCCACCCCCA 454


RESULT 66
ADC26818
ID   ADC26818 standard; DNA; 1190 BP.
XX
AC   ADC26818;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human lipitor/zocor response-related SNP DNA - SEQ ID 228.
XX
KW   statin response; cytochrome p450 3A4; CYP3A4; 2D6; CYP2D6;
KW   3-hydroxy-3-methylglutaryl-coenzyme A reductase; HMGCR; atorvastatin;
KW   simvastatin; serum cholesterol level; heart attack;
KW   single nucleotide polymorphism; SNP; human; ds; lipitor; zocor.
XX
OS   Homo sapiens.
XX
PN   WO2003002721-A2.
XX
PD   09-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020847.
XX
PR   29-JUN-2001; 2001US-0301867P.
PR   07-AUG-2001; 2001US-0310783P.
PR   13-SEP-2001; 2001US-0322478P.
XX
PA   (DNAP-) DNAPRINT GENOMICS INC.
XX
PI   Frudakis T;
XX
DR   WPI; 2003-239174/23.
XX
PT   Inferring a statin response from a nucleic acid sample, by haplotype
PT   allele indicative of statin response, a decrease in total cholesterol, or
PT   in low density lipoprotein infers a statin response of the subject.
XX
PS   Example 9; SEQ ID NO 228; 323pp; English.
XX
CC   The invention relates to a novel method for inferring a statin response
CC   from a nucleic acid sample comprising identifying in the nucleic acid
CC   sample, at least one haplotype allele indicative of a statin response.
CC   The haplotype allele may comprise nucleotides of the cytochrome p450 3A4
CC   (CYP3A4) gene, nucleotides of the cytochrome p450 2D6 (CYP2D6) gene or
CC   nucleotides of the 3-hydroxy-3-methylglutaryl-coenzyme A reductase
CC   (HMGCR) gene. The method of the invention may be useful for inferring a
CC   statin response of a human subject from a nucleic acid sample, where the
CC   human subject is a Caucasian subject and the statin is atorvastatin or
CC   simvastatin. The method may also be useful for determining whether to
CC   prescribe statin to a patient with elevated serum cholesterol levels in
CC   order to prevent heart attack. The current sequence is that of the human
CC   lipitor/zocor response-related SNP DNA of the invention.
XX
SQ   Sequence 1190 BP; 230 A; 323 C; 433 G; 202 T; 0 U; 2 Other;

  Query Match             100.0%;  Score 17;  DB 10;  Length 1190;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        438 CGCATCTCCCACCCCCA 454


RESULT 67
AAD09849
ID   AAD09849 standard; DNA; 1450 BP.
XX
AC   AAD09849;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human CYP2D6 gene.
XX
KW   Polymorphism; amplification; CYP2D6; cytochrome P450; CYP; human;
KW   drug metabolism; psychiatric disorder; cardiovascular disorder; ds.
XX
OS   Homo sapiens.
XX
PN   WO200149883-A2.
XX
PD   12-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-US035186.
XX
PR   30-DEC-1999;   99US-0173699P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Katz DA,  Gentile-Davey MC,  Cornwell MJ,  Huff JB;
XX
DR   WPI; 2001-441898/47.
XX
PT   Detecting a mutation in target nucleic acid sequence in test sample, by
PT   amplifying target and standard nucleic acid sequence using primers,
PT   hybridizing probes to the products to form hybrids, and detecting
PT   hybrids.
XX
PS   Example 1; Page 30; 35pp; English.
XX
CC   The invention relates to a method for detecting polymorphism in a target
CC   nucleic acid sequence using amplification technique. The method involves
CC   amplifying the target sequence and a standard nucleic acid sequence using
CC   primers to form amplification products, hybridising a first labelled
CC   probe to the target sequence amplification product and a second labelled
CC   probe to the standard sequence amplification product, detecting the
CC   signals from the first and the second probe, and comparing the signals to
CC   determine the polymorphism. The method is useful for detecting
CC   polymorphism in various nucleic acid sequences e.g. CYP2D6 gene which is
CC   a member of cytochrome P450 (CYP) gene family. CYP2D6 plays a role in the
CC   metabolism of several drugs, including those used for treating
CC   psychiatric and cardiovascular disorders. Polymorphism in the CYP2D6 gene
CC   have varying effect on an individual's ability to metabolise drugs. The
CC   method is suitable for detecting amplification products from multiple and
CC   different types of polymorphisms on a single automated platform. The
CC   present sequence is human CYP2D6 gene
XX
SQ   Sequence 1450 BP; 270 A; 395 C; 521 G; 264 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 4;  Length 1450;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        298 CGCATCTCCCACCCCCA 314


RESULT 68
ABT33964
ID   ABT33964 standard; DNA; 2170 BP.
XX
AC   ABT33964;
XX
DT   29-MAY-2003  (first entry)
XX
DE   Human pigmentation trait-related DNA - SEQ ID No 63.
XX
KW   Human; single nucleotide polymorphism; SNP; ds; melanocortin-1 receptor;
KW   genetic pigmentation trait; MC1R; agouti signaling protein; ASIP; race;
KW   hair colour; eye colour; forensic tool.
XX
OS   Homo sapiens.
```

XX
PN WO200297047-A2.
XX
PD 05-DEC-2002.
XX
PF 28-MAY-2002; 2002WO-US016789.
XX
PR 25-MAY-2001; 2001US-0293560P.
PR 21-JUN-2001; 2001US-0300187P.
PR 07-AUG-2001; 2001US-0310781P.
PR 17-SEP-2001; 2001US-0323662P.
PR 26-OCT-2001; 2001US-0344418P.
PR 15-NOV-2001; 2001US-0334674P.
PR 02-JAN-2002; 2002US-0346303P.
XX
PA (DNAP-) DNAPRINT GENOMICS INC.
XX
PI Frudakis T;
XX
DR WPI; 2003-239091/23.
XX
PT Inferring genetic pigmentation trait such as hair/eye color or shade from
PT nucleic acid sample of human subject, by identifying a pigmentation-
PT related haplotype allele of a pigmentation gene in the sample.
XX
PS Claim 50; Page 344-346; 396pp; English.
XX
CC The invention comprises a method for inferring a genetic pigmentation
CC trait of a human. The method involves identifying a single nucleotide
CC polymorphism (SNP) in a pigmentation gene - where the pigmentation gene
CC is not melanocortin-1 receptor (MC1R) and agouti signaling protein
CC (ASIP). The method of the invention is useful for inferring a genetic
CC pigmentation trait of a human, especially for inferring the race of a
CC human subject. The method is useful for inferring a genetic pigmentation
CC trait such as hair shade or colour, or eye shade or colour of a human
CC subject. The method may be used as a forensic tool for obtaining
CC information relating to physical characteristics of a potential crime
CC victim or a perpetrator of a crime from a nucleic acid sample present at
CC a crime scene. The present human DNA sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 2170 BP; 409 A; 593 C; 776 G; 375 T; 0 U; 17 Other;

Query Match 100.0%; Score 17; DB 8; Length 2170;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 1978 CGCATCTCCCACCCCCA 1994

RESULT 69
ABT33965
ID ABT33965 standard; DNA; 2170 BP.
XX
AC ABT33965;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human pigmentation trait-related DNA - SEQ ID No 64.
XX
KW Human; single nucleotide polymorphism; SNP; ds; melanocortin-1 receptor;
KW genetic pigmentation trait; MC1R; agouti signaling protein; ASIP; race;
KW hair colour; eye colour; forensic tool.
XX
OS Homo sapiens.
XX
PN WO200297047-A2.
XX
PD 05-DEC-2002.
XX
PF 28-MAY-2002; 2002WO-US016789.
XX
PR 25-MAY-2001; 2001US-0293560P.
PR 21-JUN-2001; 2001US-0300187P.
PR 07-AUG-2001; 2001US-0310781P.
PR 17-SEP-2001; 2001US-0323662P.
PR 26-OCT-2001; 2001US-0344418P.
PR 15-NOV-2001; 2001US-0334674P.
PR 02-JAN-2002; 2002US-0346303P.
XX
PA (DNAP-) DNAPRINT GENOMICS INC.
XX
PI Frudakis T;
XX
DR WPI; 2003-239091/23.
XX
PT Inferring genetic pigmentation trait such as hair/eye color or shade from
PT nucleic acid sample of human subject, by identifying a pigmentation-
PT related haplotype allele of a pigmentation gene in the sample.
XX
PS Claim 50; Page 346-347; 396pp; English.
XX
CC The invention comprises a method for inferring a genetic pigmentation
CC trait of a human. The method involves identifying a single nucleotide
CC polymorphism (SNP) in a pigmentation gene - where the pigmentation gene
CC is not melanocortin-1 receptor (MC1R) and agouti signaling protein
CC (ASIP). The method of the invention is useful for inferring a genetic
CC pigmentation trait of a human, especially for inferring the race of a
CC human subject. The method is useful for inferring a genetic pigmentation
CC trait such as hair shade or colour, or eye shade or colour of a human
CC subject. The method may be used as a forensic tool for obtaining
CC information relating to physical characteristics of a potential crime
CC victim or a perpetrator of a crime from a nucleic acid sample present at
CC a crime scene. The present human DNA sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 2170 BP; 409 A; 593 C; 776 G; 375 T; 0 U; 17 Other;

Query Match 100.0%; Score 17; DB 8; Length 2170;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 1978 CGCATCTCCCACCCCCA 1994

RESULT 70
ADJ78569
ID ADJ78569 standard; DNA; 4375 BP.
XX
AC ADJ78569;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human cytochrome P450 isoenzyme 2D6 pseudogene SeqID7.
XX
KW primer set; variant identification; cytochrome P450 isoenzyme 2D6;
KW CYP2D6; chromosome 22q13.1; single nucleotide polymorphism; SNP;
KW low frequency variant; pharmaceutical drugs metabolism; human;
KW pseudogene; ds.
XX
OS Homo sapiens.
XX
PN WO2004009760-A2.
XX
PD 29-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021468.
XX
PR 18-JUL-2002; 2002US-0397010P.
XX
PA (BIOV-) BIOVENTURES INC.
XX

PI Dawson EP;
XX
DR WPI; 2004-132938/13.
XX
PT New primer set useful for screening a polynucleotide sample to detect and
PT identify variants in the cytochrome P450 isoenzyme 2D6 gene, and for
PT detecting low frequency variants affecting pharmaceutical drugs
PT metabolism.
XX
PS Disclosure; SEQ ID NO 7; 51pp; English.
XX
CC This invention relates to novel primer sets that can be used to screen a
CC polynucleotide sample to detect and identify variants in the cytochrome
CC P450 isoenzyme 2D6 (CYP2D6) gene. The gene is located on chromosome
CC 22q13.1 and contains several single nucleotide polymorphisms, the details
CC of which are disclosed in the specification. The methods and compositions
CC of the present invention are useful for screening a polynucleotide sample
CC to detect and identify variants in the cytochrome P450 isoenzyme 2D6 gene
CC and detecting low frequency variants affecting pharmaceutical drugs
CC metabolism. The present sequence is that of a human cytochromome p450
CC isoenzyme 2D6 pseudogene which was used during the design of the primer
CC sets of the invention to ensure specific amplification of the correct
CC gene sequence.
XX
SQ Sequence 4375 BP; 806 A; 1265 C; 1500 G; 804 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 4375;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 1905 CGCATCTCCCACCCCCA 1921

RESULT 71
ADM28897
ID ADM28897 standard; DNA; 4375 BP.
XX
AC ADM28897;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human pseudogene #4 located near CYP2D6 gene.
XX
KW Human; cytochrome P450 isoenzyme 2D6; CYP2D6 isoenzyme;
KW altered metabolism; chromosome 22q; ds.
XX
OS Homo sapiens.
XX
PN US2004072235-A1.
XX
PD 15-APR-2004.
XX
PF 12-NOV-2003; 2003US-00712363.
XX
PR 20-JUL-2001; 2001US-0306675P.
PR 18-JUL-2002; 2002US-00360790.
PR 09-JUL-2003; 2003WO-US021468.
XX
PA (DAWS/) DAWSON E P.
XX
PI Dawson EP;
XX
DR WPI; 2004-328568/30.
XX
PT Novel primer set for screening a polynucleotide sample to detect and
PT identify variants in the cytochrome P450 isoenzyme 2D6 (CYP2D6) gene in a
PT polynucleotide sample or a population.
XX
PS Disclosure; SEQ ID NO 7; 47pp; English.
XX
CC The present invention relates to a primer set that can be used to screen
CC a polynucleotide sample to detect and identify variants in the human
CC cytochrome P450 isoenzyme 2D6 (CYP2D6) gene. Also disclosed is a kit for
CC the above screening method, a method for predicting the potential for
CC altered metabolism of a substance, including one or more than one
CC pharmaceutical drug, by a first individual compared to a second control
CC individual, where the substance is metabolised by the CYP2D6 isoenzyme, a
CC purified or isolated variant of wild-type CYP2D6 isoenzyme having one or
CC more than one of the alterations chosen from F-I at position 120, F-F at
CC position 120, E-K at position 155, R-R at position 194, F-F at position
CC 219, L-L at position 276, H-H at position 324, R-STOP at position 344, Y-
CC C at position 355, H-H at position 361, V-FRAMESHIFT at position 363, E-K
CC at position 418, H-Y at position 478 and F-F at position 483. The primer
CC set is useful for screening a polynucleotide sample to detect and
CC identify the presence of one or more than one variant in the CYP2D6 gene
CC in the sample. The primer set permits amplification from a small
CC polynucleotide sample of selected portions of the coding portion of the
CC CYP2D6 gene, or amplification of the entire coding portion of CYP2D6, as
CC well as the flanking intronic sequences that are relevant to recognition
CC of splice sites. The primer set further permits the detection of genetic
CC variants of CYP2D6 without interference from pseudogenes or from
CC homologous or paralogous genes of non-CYP2D6 cytochrome p450 genes. The
CC primer set also permits the detection of low frequency variants that
CC affect pharmaceutical drugs metabolism, thereby decreasing the false
CC negative rate in variant screening. The present sequence represents a
CC human pseudogene located on chromosome 22q near the CYP2D6 gene.
XX
SQ Sequence 4375 BP; 806 A; 1265 C; 1500 G; 804 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 4375;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 1905 CGCATCTCCCACCCCCA 1921

RESULT 72
ADB25775
ID ADB25775 standard; DNA; 4500 BP.
XX
AC ADB25775;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human CYP2D6-related DNA sequence.
XX
KW human; mutant CYP2D6 gene; drug analysis; drug testing; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003050282-A1.
XX
PD 19-JUN-2003.
XX
PF 05-DEC-2002; 2002WO-JP012748.
XX
PR 06-DEC-2001; 2001JP-00372548.
XX
PA (TSUR) TSUMURA & CO.
XX
PI Taniyama M, Ogawa K, Tsuchiya N, Hibino T;
XX
DR WPI; 2003-505401/47.
XX
PT Genetic polymorphisms of CYP2D6 gene in human population for analysis of
PT drug effect on individual patients and testing of new drugs.
XX
PS Claim 1; Page 36-39; 75pp; Japanese.
XX
CC The invention comprises mutant forms of the human CYP2D6 gene, containing
CC one or more of the following mutations G125A, C1858T, T2874C and C2875T.
CC The mutant human CYP2D6 genes of the invention are useful for analysing

```
CC   the effect of drugs on individual patients and testing of new drugs. The
CC   present DNA sequence represents a human gene of the invention.
XX
SQ   Sequence 4500 BP; 855 A; 1308 C; 1502 G; 835 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 8;  Length 4500;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       1829 CGCATCTCCCACCCCCA 1845


RESULT 73
ADS89487/c
ID   ADS89487 standard; DNA; 6001 BP.
XX
AC   ADS89487;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Oligonucleotide of the invention SEQ ID NO:503.
XX
KW   ss; cell proliferative disorder; breast; methylation; cytostatic;
KW   gene therapy; single nucleotide polymorphism; SNP.
XX
OS   Unidentified.
XX
PN   WO2004035803-A2.
XX
PD   29-APR-2004.
XX
PF   01-OCT-2003; 2003WO-EP010881.
XX
PR   01-OCT-2002; 2002DE-01045779.
PR   07-JAN-2003; 2003DE-01000096.
PR   17-APR-2003; 2003DE-01017955.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Foekens J,  Harbeck N,  Koenig T,  Maier S,  Martens J,  Model F;
PI   Nimmrich I,  Rujan T,  Schmitt A,  Schmitt M,  Look MP,  Marx A;
XX
DR   WPI; 2004-348468/32.
XX
PT   Predicting responsiveness of a subject with breast cell proliferative
PT   disorder, useful for treating or differentiating breast cell
PT   proliferative disorders comprises analyzing methylation pattern of a
PT   genomic DNA from the subject.
XX
PS   Claim 25; SEQ ID NO 503; 104pp;. English.
XX
CC   The invention relates to a novel method for predicting the responsiveness
CC   of a subject with a cell proliferative disorder of the breast tissues to
CC   a therapy comprising analysing the methylation pattern of a target
CC   nucleic acid by contacting at least one of the target nucleic acids in a
CC   biological sample obtained from the subject prior to or during treatment.
CC   The method of the invention has cytostatic activity, and may have a use
CC   in gene therapy. The set of oligonucleotides comprising at least two of
CC   the oligomers are useful for detecting the cytosine methylation state
CC   and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC   methods, nucleic acid, oligonucleotide, and kit are useful for the
CC   treatment, characterisation, classification and/or differentiation, of
CC   breast cell proliferative disorders. The method is also useful for
CC   predicting the responsiveness of a subject with a cell proliferative
CC   disorder of the breast tissues to a therapy. The present sequence is used
CC   in the exemplification of the invention.
XX
SQ   Sequence 6001 BP; 1144 A; 217 C; 1679 G; 2961 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 13;  Length 6001;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3105 CGCATCTCCCACCCCCA 3089


RESULT 74
ADS89113/c
ID   ADS89113 standard; DNA; 6001 BP.
XX
AC   ADS89113;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human CYP2D6 gene SEQ ID NO:129.
XX
KW   ds; gene; human; cell proliferative disorder; breast; methylation;
KW   cytostatic; gene therapy; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
PN   WO2004035803-A2.
XX
PD   29-APR-2004.
XX
PF   01-OCT-2003; 2003WO-EP010881.
XX
PR   01-OCT-2002; 2002DE-01045779.
PR   07-JAN-2003; 2003DE-01000096.
PR   17-APR-2003; 2003DE-01017955.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Foekens J,  Harbeck N,  Koenig T,  Maier S,  Martens J,  Model F;
PI   Nimmrich I,  Rujan T,  Schmitt A,  Schmitt M,  Look MP,  Marx A;
XX
DR   WPI; 2004-348468/32.
XX
PT   Predicting responsiveness of a subject with breast cell proliferative
PT   disorder, useful for treating or differentiating breast cell
PT   proliferative disorders comprises analyzing methylation pattern of a
PT   genomic DNA from the subject.
XX
PS   Claim 15; SEQ ID NO 129; 104pp; English.
XX
CC   The invention relates to a novel method for predicting the responsiveness
CC   of a subject with a cell proliferative disorder of the breast tissues to
CC   a therapy comprising analysing the methylation pattern of a target
CC   nucleic acid by contacting at least one of the target nucleic acids in a
CC   biological sample obtained from the subject prior to or during treatment.
CC   The method of the invention has cytostatic activity, and may have a use
CC   in gene therapy. The set of oligonucleotides comprising at least two of
CC   the oligomers are useful for detecting the cytosine methylation state
CC   and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC   methods, nucleic acid, oligonucleotide, and kit are useful for the
CC   treatment, characterisation, classification and/or differentiation, of
CC   breast cell proliferative disorders. The method is also useful for
CC   predicting the responsiveness of a subject with a cell proliferative
CC   disorder of the breast tissues to a therapy. The present sequence is used
CC   in the exemplification of the invention.
XX
SQ   Sequence 6001 BP; 1144 A; 2003 C; 1679 G; 1175 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 13;  Length 6001;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3105 CGCATCTCCCACCCCCA 3089
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RESULT 75
ABQ72215
ID   ABQ72215 standard; DNA; 6472 BP.
XX
AC   ABQ72215;
XX
DT   02-SEP-2002  (first entry)
XX
DE   Human CYP2D6 gene, SEQ ID NO:1 version #1.
XX
KW   Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme;
KW   chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase;
KW   antiarrhythmic; arrhythmia; adrenoreceptor antagonist; hypertension;
KW   tricyclic antidepressant; procainamide; drug induced lupus syndrome;
KW   environmentally linked disease; Parkinsons's disease; haplotyping;
KW   genotyping; haplotype; genetic variant; single nucleotide polymorphism;
KW   SNP; drug screening; drug discovery; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(636, A)
FT                   /*tag= a
FT                   /label= PS1
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as R in the specification"
FT   variation       replace(678, C)
FT                   /*tag= b
FT                   /label= PS2
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification"
FT   variation       replace(769, C)
FT                   /*tag= c
FT                   /label= PS3
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as S in the specification"
FT   variation       replace(776, G)
FT                   /*tag= d
FT                   /label= PS4
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as R in the specification"
FT   variation       replace(825, A)
FT                   /*tag= e
FT                   /label= PS5
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as R in the specification"
FT   variation       replace(915, C)
FT                   /*tag= f
FT                   /label= PS6
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification"
FT   CDS             1001. .5217
FT                   /*tag= g
FT                   /product= "CYP2D6"
FT   exon            1001. .1180
FT                   /*tag= h
FT                   /number= 1
FT   variation       replace(1019, A)
FT                   /*tag= i
FT                   /label= PS7
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as R in the specification; causes the amino acid
FT                   substitution V7M"
FT   variation       replace(1031, A)
FT                   /*tag= j
FT                   /label= PS8
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as R in the specification; causes the amino acid
FT                   substitution V11M"
FT   variation       replace(1100, T)
FT                   /*tag= k
FT                   /label= PS9
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as Y in the specification; causes the amino acid
FT                   substitution P34S"
FT   intron          1181. .1883
FT                   /*tag= l
FT                   /number= 1
FT   variation       replace(1827, C)
FT                   /*tag= m
FT                   /label= PS10
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as S in the specification"
FT   variation       replace(1843, G)
FT                   /*tag= n
FT                   /label= PS11
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as K in the specification"
FT   exon            1884. .2055
FT                   /*tag= o
FT                   /number= 2
FT   variation       replace(1966, A)
FT                   /*tag= p
FT                   /label= PS12
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as R in the specification; causes the amino acid
FT                   substitution R88H"
FT   variation       replace(1974, A)
FT                   /*tag= q
FT                   /label= PS13
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as M in the specification; causes the amino acid
FT                   substitution L91M"
FT   variation       replace(1984, G)
FT                   /*tag= r
FT                   /label= PS14
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as R in the specification; causes the amino acid
FT                   substitution H94R"
FT   variation       replace(1997, G)
FT                   /*tag= s
FT                   /label= PS15
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as S in the specification"
FT   variation       replace(2014, C)
FT                   /*tag= t
FT                   /label= PS16
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification; causes the amino acid
FT                   substitution V104A"
FT   variation       replace(2022, T)
FT                   /*tag= u
FT                   /label= PS17
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as W in the specification; together with PS18 causes the
FT                   amino acid substitution T107F"
FT   variation       replace(2023, T)
FT                   /*tag= v
FT                   /label= PS18
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification; together with PS17 causes the
FT                   amino acid substitution T107F"
FT   variation       replace(2028, G)
FT                   /*tag= w
FT                   /label= PS19
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as R in the specification; causes the amino acid
FT                   substitution I109V"
FT   variation       replace(2036, C)
FT                   /*tag= x
FT                   /label= PS20
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification"
FT   variation       replace(2039, T)
FT                   /*tag= y
FT                   /label= PS21
```

```
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as Y in the specification"
FT   intron          2056. .2605
FT                   /*tag= z
FT                   /number= 2
FT                   /cons_splice= (5'site:NO, 3'site:YES)
FT   variation       replace(2062, G)
FT                   /*tag= aa
FT                   /label= PS22
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as R in the specification"
FT   variation       replace(2067, G)
FT                   /*tag= ab
FT                   /label= PS23
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as K in the specification"
FT   variation       replace(2118, T)
FT                   /*tag= ac
FT                   /label= PS24
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification"
FT   variation       replace(2170, A)
FT                   /*tag= ad
FT                   /label= PS25
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as R in the specification"
FT   variation       replace(2179, C)
FT                   /*tag= ae
FT                   /label= PS26
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as S in the specification"
FT   exon            2606. .2758
FT                   /*tag= af
FT                   /number= 3
FT   variation       replace(2611, A)
FT                   /*tag= ag
FT                   /label= PS27
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as W in the specification; causes the amino acid
FT                   substitution F120I"
FT   variation       replace(2635, C)
FT                   /*tag= ah
FT                   /label= PS28
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification; causes the amino acid
FT                   substitution W128R"
FT   variation       replace(2659, A)
FT                   /*tag= ai
FT                   /label= PS29
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as R in the specification; together with PS30 causes the
FT                   amino acid substitution V136I"
FT   variation       replace(2661, C)
FT                   /*tag= aj
FT                   /label= PS30
FT                   /note= "Known single nucleotide polymorphism (SNP); given

  Query Match             100.0%;  Score 17;  DB 6;  Length 6472;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       2829 CGCATCTCCCACCCCCA 2845


RESULT 76
ABQ72364
ID   ABQ72364 standard; DNA; 6472 BP.
XX
AC   ABQ72364;
XX
DT   02-SEP-2002  (first entry)

XX
DE   Human CYP2D6 gene, SEQ ID NO:1 version #2.
XX
KW   Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme;
KW   chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase;
KW   antiarrhythmic; arrhythmia; adrenoreceptor antagonist; hypertension;
KW   tricyclic antidepressant; procainamide; drug induced lupus syndrome;
KW   environmentally linked disease; Parkinsons's disease; haplotyping;
KW   genotyping; haplotype; genetic variant; single nucleotide polymorphism;
KW   SNP; drug screening; drug discovery; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(636, A)
FT                   /*tag= a
FT                   /label= PS1
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(678, C)
FT                   /*tag= b
FT                   /label= PS2
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(769, C)
FT                   /*tag= c
FT                   /label= PS3
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(776, G)
FT                   /*tag= d
FT                   /label= PS4
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(825, A)
FT                   /*tag= e
FT                   /label= PS5
FT                   /note= "Known single nucleotide polymorphism (SNP)"
FT   variation       replace(915, C)
FT                   /*tag= f
FT                   /label= PS6
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   CDS             1001. .5217
FT                   /*tag= g
FT                   /product= "CYP2D6"
FT   exon            1001. .1180
FT                   /*tag= h
FT                   /number= 1
FT   variation       replace(1019, A)
FT                   /*tag= i
FT                   /label= PS7
FT                   /note= "Known single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution V7M"
FT   variation       replace(1031, A)
FT                   /*tag= j
FT                   /label= PS8
FT                   /note= "Known single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution V11M"
FT   variation       replace(1100, T)
FT                   /*tag= k
FT                   /label= PS9
FT                   /note= "Known single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution P34S"
FT   intron          1181. .1883
FT                   /*tag= l
FT                   /number= 1
FT   variation       replace(1827, C)
FT                   /*tag= m
FT                   /label= PS10
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(1843, G)
FT                   /*tag= n
FT                   /label= PS11
FT                   /note= "Known single nucleotide polymorphism (SNP)"
FT   exon            1884. .2055
FT                   /*tag= o
FT                   /number= 2
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FT   variation       replace(1966, A)
FT                   /*tag= p
FT                   /label= PS12
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution R88H"
FT   variation       replace(1974, A)
FT                   /*tag= q
FT                   /label= PS13
FT                   /note= "Known single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution L91M"
FT   variation       replace(1984, G)
FT                   /*tag= r
FT                   /label= PS14
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution H94R"
FT   variation       replace(1997, G)
FT                   /*tag= s
FT                   /label= PS15
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(2014, C)
FT                   /*tag= t
FT                   /label= PS16
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution V104A"
FT   variation       replace(2022, T)
FT                   /*tag= u
FT                   /label= PS17
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   together with PS18 causes the amino acid substitution
FT                   T107F"
FT   variation       replace(2023, T)
FT                   /*tag= v
FT                   /label= PS18
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   together with PS17 causes the amino acid substitution
FT                   T107F"
FT   variation       replace(2028, G)
FT                   /*tag= w
FT                   /label= PS19
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution I109V"
FT   variation       replace(2036, C)
FT                   /*tag= x
FT                   /label= PS20
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(2039, T)
FT                   /*tag= y
FT                   /label= PS21
FT                   /note= "Known single nucleotide polymorphism (SNP)"
FT   intron          2056. .2605
FT                   /*tag= z
FT                   /number= 2
FT                   /cons_splice= (5'site:NO, 3'site:YES)
FT   variation       replace(2062, G)
FT                   /*tag= aa
FT                   /label= PS22
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(2067, G)
FT                   /*tag= ab
FT                   /label= PS23
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(2118, T)
FT                   /*tag= ac
FT                   /label= PS24
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(2170, A)
FT                   /*tag= ad
FT                   /label= PS25
FT                   /note= "Known single nucleotide polymorphism (SNP)"
FT   variation       replace(2179, C)
FT                   /*tag= ae
FT                   /label= PS26
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   exon            2606. .2758
FT                   /*tag= af
FT                   /number= 3
FT   variation       replace(2611, A)
FT                   /*tag= ag
FT                   /label= PS27
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution F120I"
FT   variation       replace(2635, C)
FT                   /*tag= ah
FT                   /label= PS28
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution W128R"
FT   variation       replace(2659, A)
FT                   /*tag= ai
FT                   /label= PS29
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   together with PS30 causes the amino acid substitution
FT                   V136I"
FT   variation       replace(2661, C)
FT                   /*tag= aj
FT                   /label= PS30
FT                   /note= "Known single nucleotide polymorphism (SNP);
FT                   together with PS29 causes the amino acid substitution
FT                   V136I"
FT   variation       replace(2704, G)
FT                   /*tag= ak
FT                   /label= PS31
FT                   /note= "Known single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution Q151E"
FT   variation       replace(2716, A)
FT                   /*tag= al
FT                   /label= PS32
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution E155K"
FT   intron          2759. .2846
FT                   /*tag= am
FT                   /number= 3
FT   variation       replace(2846, A)
FT                   /*tag= an
FT                   /label= PS33
FT                   /note= "Known single nucleotide polymorphism (SNP)"
FT   exon            2847. .3007
FT                   /*tag= ao
FT                   /number= 4
FT   intron          3008. .3440
FT                   /*tag= ap
FT                   /number= 4
FT   variation       replace(3292, A)

  Query Match             100.0%;  Score 17;  DB 6;  Length 6472;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       2829 CGCATCTCCCACCCCCA 2845


RESULT 77
AAD34213
ID   AAD34213 standard; DNA; 9432 BP.
XX
AC   AAD34213;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human cytochrome P450 2D6 (CYP2D6) gene.
XX
KW   Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
KW   ligase-based sequenced determination; drug metabolism; chromosome 22;
KW   gene; ds.
XX
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OS   Homo sapiens.
XX
PN   WO200218638-A2.
XX
PD   07-MAR-2002.
XX
PF   27-AUG-2001; 2001WO-IB001544.
XX
PR   30-AUG-2000; 2000GB-00021286.
XX
PA   (GEMI-) GEMINI GENOMICS PLC.
XX
PI   Risinger C,  Andersson MK,  Lewander T,  Oliasson E;
XX
DR   WPI; 2002-329785/36.
XX
PT   New sequence determination oligonucleotides, useful for detecting
PT   polymorphic sites in a 5' flanking region of a CYP2D6 gene, as
PT   hybridization probes, as components of diagnostic assays, or in ligase-
PT   based sequence determination.
XX
PS   Example 3; Fig 1; 63pp; English.
XX
CC   The invention relates to sequence determination oligonucleotides for
CC   detecting polymorphic sites in a 5' flanking region of cytochrome P450
CC   2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many
CC   different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The
CC   oligonucleotides may be used as in situ hybridisation probes, in ligase-
CC   based sequenced determination, as components of diagnostic assays, as
CC   probes in sequence determination methods based on mismatches, as
CC   hybridisation-based diagnostic assays, and as components of diagnostic
CC   microarray. CYP2D6 is useful to predict variations in an individual's
CC   ability to metabolise certain drugs. The present sequence is human CYP2D6
CC   gene
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 6;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 78
ACA61301
ID   ACA61301 standard; DNA; 9432 BP.
XX
AC   ACA61301;
XX
DT   16-JUL-2003  (first entry)
XX
DE   Human cytochrome p450 gene CYP2D6, wild-type.
XX
KW   Human; ds; gene; cytochrome P450; CYP2D6; chromosome 22; SNP;
KW   single nucleotide polymorphism; drug metabolism; cardiovascular disorder;
KW   psychiatric disorder; drug sensitivity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(226. .227,ATT)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(971,G)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1111,T)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1726,C)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1846,A)
FT                   /*tag=  f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1846,G)
FT                   /*tag=  e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(2064,A)
FT                   /*tag=  g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3023,A)
FT                   /*tag=  h
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5799,C)
FT                   /*tag=  i
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5816,TA)
FT                   /*tag=  j
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1281755-A2.
XX
PD   05-FEB-2003.
XX
PF   16-JUL-2002; 2002EP-00254972.
XX
PR   31-JUL-2001; 2001US-0309111P.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Milos PM,  Webb SM;
XX
DR   WPI; 2003-373769/36.
XX
PT   New cytochrome P450 2D6 gene variants and polypeptides, useful for
PT   determining if a subject has or is at risk of developing a drug
PT   sensitivity condition or disorder that is associated with an aberrant
PT   CYP2D6 activity.
XX
PS   Claim 1; Fig 2; 88pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising a cytochrome
CC   P450 2D6 gene variant, e.g. G5799C or C5816AT (referring to the genomic
CC   sequence or the same variant nucleotide in the corresponding cDNA
CC   sequences). Also included are probes, primers (allele specific
CC   oligonucleotides) and arrays used to detect and or amplify the CYP2D6
CC   gene polymorphic regions, the variant polypeptides, antibodies which are
CC   capable of distinguishing between the variant and wild-type polypeptides,
CC   determining whether a subject has a genetic deficiency for metabolising a
CC   drug, evaluating therapy with a drug metabolised by P450 CYP2D6 and
CC   determining whether an individual is susceptible to being a poor
CC   metaboliser of drugs. The DNA probe is useful for hybrisiding to a
CC   variant form of the CYP2D6 gene. The primer is useful for amplifying the
CC   C5816TA allelic variant. The allele specific nucleotide is useful for the
CC   detection of the C5816TA allelic variant. The methods are useful for
CC   determining whether a subject has a genetic deficiency for metabolising a
CC   drug, evaluating therapy with a drug metabolised by P450 CYP2D6, and
CC   determining if an individual is susceptible to being a poor metaboliser
CC   of drugs. The nucleic acids are useful as probes or primers for
CC   determining whether a subject has a genetic deficiency for metabolising
CC   drugs that are substrates of P450 CYP2D6. The methods are useful for
CC   determining if a subject has or is at risk of developing a drug
CC   sensitivity condition or disorder that is associated with an aberrant
CC   CYP2D6 activity, e.g. an aberrant level of a CYP2D6 protein or an
CC   aberrant CYP2D6 bioactivity. The methods are also useful in selecting the
CC   appropriate drugs or determining the course of treatment to administer to
CC   a subject to treat cardiovascular or psychiatric disorders, or for
CC   treating a subject with a drug sensitivity or disorder associated with a
CC   specific allelic variant of a polymorphic region of the CYP2D6 gene. The
CC   antibodies are useful for monitoring CYP2D6 protein levels in an
CC   individual for determining whether a subject has a disease or conditions
CC   associated with an aberrant CYP2D6 protein level. The gene is located on
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CC   human chromosome 22. The present sequence is the wild-type CYP2D6 gene
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 17;  DB 10;  Length 9432;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 79
ADF83400
ID   ADF83400 standard; DNA; 9432 BP.
XX
AC   ADF83400;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CYP2D6 gene (wild-type).
XX
KW   Human; antiemetic; setrone; cytochrome P450; CYP2D6; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1620. .5836
FT                   /*tag= b
FT                   /product= "CYP2D6"
FT   exon            1620. .1799
FT                   /*tag= a
FT   variation       replace(1719,t)
FT                   /*tag= c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1743,a)
FT                   /*tag= d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1756. .1757,ttg)
FT                   /*tag= e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   intron          1800. .2502
FT                   /*tag= f
FT   variation       replace(2502,c)
FT                   /*tag= g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   exon            2503. .2674
FT                   /*tag= h
FT   intron          2675. .3224
FT                   /*tag= i
FT                   /cons_splice= (5'site:NO, 3'site:YES)
FT   exon            3225. .3377
FT                   /*tag= j
FT   variation       replace(3325. .3327,gg)
FT                   /*tag= k
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3377,t)
FT                   /*tag= l
FT                   /standard_name= "Single nucleotide polymorphism"
FT   intron          3378. .3465
FT                   /*tag= m
FT   variation       replace(3465,a)
FT                   /*tag= n
FT                   /standard_name= "Single nucleotide polymorphism"
FT   exon            3466. .3626
FT                   /*tag= o
FT   intron          3627. .4059
FT                   /*tag= p
FT   exon            4060. .4236
FT                   /*tag= q
FT   variation       replace(4167. .4169,cg)
FT                   /*tag= r
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4231. .4235,ga)
FT                   /*tag= s
FT                   /standard_name= "Single nucleotide polymorphism"
FT   intron          4237. .4426
FT                   /*tag= t
FT   exon            4427. .4568
FT                   /*tag= u
FT   variation       replace(4469,t)
FT                   /*tag= v
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4554,c)
FT                   /*tag= w
FT                   /standard_name= "Single nucleotide polymorphism"
FT   intron          4569. .4775
FT                   /*tag= x
FT   exon            4776. .4963
FT                   /*tag= y
FT   intron          4964. .5417
FT                   /*tag= z
FT   exon            5418. .5559
FT                   /*tag= aa
FT   intron          5560. .5657
FT                   /*tag= ab
FT   exon            5658. .5836
FT                   /*tag= ac
FT   variation       replace(5799,c)
FT                   /*tag= ad
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO2003100091-A1.
XX
PD   04-DEC-2003.
XX
PF   22-MAY-2003; 2003WO-EP005366.
XX
PR   24-MAY-2002; 2002EP-00011491.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Brockmoeller HJ;
XX
DR   WPI; 2004-035165/03.
DR   P-PSDB; ADF83401.
DR   GENBANK; GI_181303.
XX
PT   Use of setrones for preparing a pharmaceutical composition for treating
PT   or preventing setrone-treatable diseases in a subject having in its
PT   genome less than three copies of a polynucleotide encoding a functional
PT   CYP2D6 polypeptide.
XX
PS   Disclosure; SEQ ID NO 50; 153pp; English.
XX
CC   The present sequence comprises the human cytochrome P450 CYP2D6 wild-type
CC   gene. CYP2D6 polymorphisms serve as genetic markers for CYP2D6 metabolic
CC   capacity. The invention relates to the use of setrones (antiemetics) for
CC   treating and/or preventing setrone-treatable diseases in a subject having
CC   in its genome fewer than 3 copies of a polynucleotide encoding a
CC   functional CYP2D6 polypeptide. The subject has at least one first variant
CC   allele selected from: CYP2D6*3, CYP2D6*4, CYP2D6*5, CYP2D6*6, CYP2D6*7,
CC   CYP2D6*8, CYP2D6*11, CYP2D6*12 and CYP2D6*15, and preferably has at least
CC   one first variant allele selected from: CYP2D6*1, CYP2D6*2, CYP2D6*9 and
CC   CYP2D6*10. The variant allele results in altered (decreased) expression.
CC   The treatment regimen can be modified according to the genotype of the
CC   subject's CYP2D6 and/or HTR3B gene. Non-responders to antiemetic therapy
CC   can be identified on a pharmacogenetic basis, allowing a suitable therapy
CC   to be selected. The setrone-treatable diseases are postoperative nausea
CC   and/or vomiting, or nausea and/or vomiting secondary to cancer
CC   chemotherapy, radiation therapy, migraine, acetaminophen poisoning,
CC   prostacyclin therapy, and opioid treatment, spinal or epidural opioid-
CC   related pruritus, acute levodopa-induced psychosis, bulimia nervosa,
CC   fibromyalgia, chronic fatigue syndrome, obsessive-compulsive disorders,
CC   schizophrenia, alcoholism, cocaine addiction, opioid withdrawal syndrome,
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CC   drug withdrawal phenomena, anxiety disorders, cognitive disturbances,
CC   neuroleptic-induced tardive dyskinesia, Tourette's syndrome, migraine
CC   headache or gastrointestinal motility disorder (all claimed).
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 80
ADJ78563
ID   ADJ78563 standard; DNA; 9432 BP.
XX
AC   ADJ78563;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human cytochrome P450 isoenzyme 2D6 genomic gene sequence SeqID1.
XX
KW   primer set; variant identification; cytochrome P450 isoenzyme 2D6;
KW   CYP2D6; chromosome 22q13.1; single nucleotide polymorphism; SNP;
KW   low frequency variant; pharmaceutical drugs metabolism; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(1522,T)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1576,GG)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1851,C)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1852,C)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1864,G)
FT                   /*tag=  e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3230,A)
FT                   /*tag=  f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3232,T)
FT                   /*tag=  g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3335,A)
FT                   /*tag=  h
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3542,T)
FT                   /*tag=  i
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3617,C)
FT                   /*tag=  j
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3716,G)
FT                   /*tag=  k
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3922,T)
FT                   /*tag=  l
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4221,T)
FT                   /*tag=  m
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4280,A)
FT                   /*tag=  n
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4282,A)
FT                   /*tag=  o
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4379,A)
FT                   /*tag=  p
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4555,C)
FT                   /*tag=  q
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4607,A)
FT                   /*tag=  r
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4820,T)
FT                   /*tag=  s
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4854,G)
FT                   /*tag=  t
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4873,C)
FT                   /*tag=  u
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4878,TGT)
FT                   /*tag=  v
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5003,A)
FT                   /*tag=  w
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5027,C)
FT                   /*tag=  x
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5054,A)
FT                   /*tag=  y
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5409,T)
FT                   /*tag=  z
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5496,A)
FT                   /*tag=  aa
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5774,T)
FT                   /*tag=  ab
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5791,T)
FT                   /*tag=  ac
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5948,T)
FT                   /*tag=  ad
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(6020,T)
FT                   /*tag=  ae
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO2004009760-A2.
XX
PD   29-JAN-2004.
XX
PF   09-JUL-2003; 2003WO-US021468.
XX
PR   18-JUL-2002; 2002US-0397010P.
XX
PA   (BIOV-) BIOVENTURES INC.
XX
PI   Dawson EP;
XX
DR   WPI; 2004-132938/13.
DR   P-PSDB; ADJ78565.
XX
PT   New primer set useful for screening a polynucleotide sample to detect and
PT   identify variants in the cytochrome P450 isoenzyme 2D6 gene, and for
PT   detecting low frequency variants affecting pharmaceutical drugs
PT   metabolism.
XX
```

PS Claim 11; SEQ ID NO 1; 51pp; English.
XX
CC This invention relates to novel primer sets that can be used to screen a
CC polynucleotide sample to detect and identify variants in the cytochrome
CC P450 isoenzyme 2D6 (CYP2D6) gene. The gene is located on chromosome
CC 22q13.1 and contains several single nucleotide polymorphisms, the details
CC of which are disclosed in the specification. The methods and compositions
CC of the present invention are useful for screening a polynucleotide sample
CC to detect and identify variants in the cytochrome P450 isoenzyme 2D6 gene
CC and detecting low frequency variants affecting pharmaceutical drugs
CC metabolism. The present sequence is that of the gene which encodes the
CC wild-type human cytochrome P450 isoenzyme 2D6 protein and which is
CC related to the invention. Note: This sequence contains introns, the
CC number and location of which are not disclosed within the specification.
CC As well as the featured SNPs, an exon 9 gene conversion is also claimed
CC in claim 25 of the specification.
XX
SQ Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 9432;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 3448 CGCATCTCCCACCCCCA 3464

RESULT 81
ADM28891
ID ADM28891 standard; DNA; 9432 BP.
XX
AC ADM28891;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human wild-type CYP2D6 gene sequence.
XX
KW Human; cytochrome P450 isoenzyme 2D6; CYP2D6 isoenzyme;
KW altered metabolism; chromosome 22q13.1; gene; ds.
XX
OS Homo sapiens.
XX
PN US2004072235-A1.
XX
PD 15-APR-2004.
XX
PF 12-NOV-2003; 2003US-00712363.
XX
PR 20-JUL-2001; 2001US-0306675P.
PR 18-JUL-2002; 2002US-00360790.
PR 09-JUL-2003; 2003WO-US021468.
XX
PA (DAWS/) DAWSON E P.
XX
PI Dawson EP;
XX
DR WPI; 2004-328568/30.
DR P-PSDB; ADM28893.
XX
PT Novel primer set for screening a polynucleotide sample to detect and
PT identify variants in the cytochrome P450 isoenzyme 2D6 (CYP2D6) gene in a
PT polynucleotide sample or a population.
XX
PS Claim 11; SEQ ID NO 1; 47pp; English.
XX
CC The present invention relates to a primer set that can be used to screen
CC a polynucleotide sample to detect and identify variants in the human
CC cytochrome P450 isoenzyme 2D6 (CYP2D6) gene. Also disclosed is a kit for
CC the above screening method, a method for predicting the potential for
CC altered metabolism of a substance, including one or more than one
CC pharmaceutical drug, by a first individual compared to a second control
CC individual, where the substance is metabolised by the CYP2D6 isoenzyme, a
CC purified or isolated variant of wild-type CYP2D6 isoenzyme having one or
CC more than one of the alterations chosen from F-I at position 120, F-F at
CC position 120, E-K at position 155, R-R at position 194, F-F at position
CC 219, L-L at position 276, H-H at position 324, R-STOP at position 344, Y-
CC C at position 355, H-H at position 361, V-FRAMESHIFT at position 363, E-K
CC at position 418, H-Y at position 478 and F-F at position 483. The primer
CC set is useful for screening a polynucleotide sample to detect and
CC identify the presence of one or more than one variant in the CYP2D6 gene
CC in the sample. The primer set permits amplification from a small
CC polynucleotide sample of selected portions of the coding portion of the
CC CYP2D6 gene, or amplification of the entire coding portion of CYP2D6, as
CC well as the flanking intronic sequences that are relevant to recognition
CC of splice sites. The primer set further permits the detection of genetic
CC variants of CYP2D6 without interference from pseudogenes or from
CC homologous or paralogous genes of non-CYP2D6 cytochrome p450 genes. The
CC primer set also permits the detection of low frequency variants that
CC affect pharmaceutical drugs metabolism, thereby decreasing the false
CC negative rate in variant screening. The present sequence represents human
CC wild-type CYP2D6 gene. The gene maps to chromosome 22q13.1.
XX
SQ Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 9432;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 3448 CGCATCTCCCACCCCCA 3464

RESULT 82
AEF35804
ID AEF35804 standard; DNA; 9432 BP.
XX
AC AEF35804;
XX
DT 23-MAR-2006 (first entry)
XX
DE Human cytochrome P450 2D6 DNA.
XX
KW diagnosis; prophylaxis; hepatitis B infection; hepatitis C infection;
KW hepatitis D infection; drug-induced hepatotoxicity; liver tumor;
KW liver cirrhosis; fibrosis; autoimmune hepatitis;
KW primary biliary cirrhosis; primary sclerosing cholangitis;
KW hemochromatosis; Wilson's disease; alpha-1 antitrypsin deficiency;
KW celiac disease; amyloidosis; gastrointestinal disease;
KW metabolic disorder; inflammation; cardiant; antiinflammatory;
KW hepatotropic; virucide; gastrointestinal-gen.; cns-gen.; metabolic;
KW immunosuppressive; cytostatic; cytochrome P450 2D6; CYP2D6; ds;
KW chromosome-22; gene.
XX
OS Homo sapiens.
XX
PN WO2006003654-A2.
XX
PD 12-JAN-2006.
XX
PF 30-JUN-2005; 2005WO-IL000700.
XX
PR 01-JUL-2004; 2004US-0584179P.
XX
PA (MEDI-) MEDICAL RES FUND TEL AVIV SOURASKY MED.
XX
PI Oren R;
XX
DR WPI; 2006-090428/09.
DR P-PSDB; AEF35802.
DR GENBANK; M33388.
XX
PT Determining if an individual is predisposed to fast progression of liver
PT fibrosis comprises determining a presence or absence of at least one fast
PT progression liver fibrosis-associated genotype.

```
XX
PS   Example 1; SEQ ID NO 6; 105pp; English.
XX
CC   The invention relates to a method of determining if an individual is
CC   predisposed to fast progression of liver fibrosis or liver cirrhosis
CC   comprising determining a presence or absence, in a homozygous or
CC   heterozygous form, of at least one fast progression liver fibrosis-
CC   associated genotype in the CYP2D6, CYP3A5, CYP2E1, or APO E locus or in
CC   neighboring loci of the individual, where the neighboring loci is in
CC   linkage disequilibrium with the locus, thus determining if the individual
CC   is predisposed to fast progression of liver fibrosis; a kit to carry out
CC   the method; a method of preventing fast progression of liver fibrosis in
CC   an individual, by upregulating CYP2D6 expression and/or activity; and a
CC   method of determining if a drug molecule is capable of inducing or
CC   accelerating development of fast progression of liver fibrosis in an
CC   individual. The individual is suffering from a hepatitis viral infection
CC   caused by hepatitis B, C or D virus, a hepatotoxicity (alcohol- or drug-
CC   induced), a liver cancer, a non-alcoholic fatty liver disease (NAFLD), an
CC   autoimmune disease (autoimmune hepatitis (AIH), primary biliary cirrhosis
CC   (PBC), or primary sclerosing cholangitis (PSC)), a metabolic liver
CC   disease (Hemochromatosis, Wilson's disease, or alpha 1 anti trypsin), or
CC   a disease with secondary involvement of the liver (celiac disease and/or
CC   amyloidosis). The method and kit are useful for determining if an
CC   individual is predisposed to fast progression of liver fibrosis. The
CC   method and drug are useful for preventing liver cirrhosis and fast
CC   progression of liver fibrosis. This sequence is human cytochrome P450 2D6
CC   DNA, located on chromosome 22q13.1.
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 15;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 83
AEF38201
ID   AEF38201 standard; DNA; 9432 BP.
XX
AC   AEF38201;
XX
DT   23-MAR-2006  (first entry)
XX
DE   Human debrisoquine 4-hydroxylase (CYP2D6) gene.
XX
KW   Drug metabolism; gene; ds; chromosome-22; cytochrome P450 2D6;
KW   debrisoquine 4-hydroxylase; SNP detection; SNP;
KW   single nucleotide polymorphism; DNA microarray.
XX
OS   Homo sapiens.
XX
PN   WO2006002526-A1.
XX
PD   12-JAN-2006.
XX
PF   30-JUN-2005; 2005WO-CA001000.
XX
PR   30-JUN-2004; 2004US-0583605P.
XX
PA   (TMBI-) TM BIOSCIENCE CORP.
XX
PI   Merante F,  Gordon JD,  Bortolin S;
XX
DR   WPI; 2006-090278/09.
XX
PT   Detecting nucleotide variants e.g. 1846G-A at polymorphic sites in gene
PT   encoding cytochrome P450-2D6, by amplifying DNA variants, hybridizing
PT   tagged extension primers to amplified DNA and to probes, detecting
PT   labeled extension products.
XX
PS   Disclosure; SEQ ID NO 1; 42pp; English.
XX
CC   The invention relates to detecting nucleotide variants chosen from -1584C
CC   -G, 1846G-A, 2549A-del at polymorphic sites in the gene encoding
CC   cytochrome P450-2D6 (encoding debrisoquine 4-hydroxylase) comprising
CC   amplifying regions of DNA containing variants, hybridizing two tagged
CC   allele specific extension primers to complementary target sequence in
CC   amplified DNA products, extending primers using labeled nucleotides,
CC   hybridizing the primers to the probe sequence and detecting the labeled
CC   extension products. Also included is a kit (I) for detecting the presence
CC   or absence of nucleotide variants at the polymorphic sites comprising a
CC   set of at least two tagged allele specific extension primers, where each
CC   tagged allele specific extension primer has a 3'-end hybridizing portion
CC   including a 3' terminal nucleotide being either complementary to a
CC   suspected variant nucleotide or to the corresponding wild-type nucleotide
CC   of one of the polymorphic sites and a 5'-end tag portion complementary to
CC   a corresponding probe sequence, and where the two tagged allele-specific
CC   extension primers are chosen from AEF38210-AEF38235 or a set of PCR
CC   amplification primers for amplifying regions of DNA containing the two
CC   polymorphic sites, appearing as AEF38202-AEF38209. The method is useful
CC   for detecting the presence or absence of nucleotide variants at
CC   polymorphic sites in the gene encoding cytochrome P450-2D6, -1584C-G,
CC   100C-G, 1023C-T, 1846G-A, 2549A-del, 2850C-T, 2935A-C, etc. The method is
CC   useful for identifying individuals who may have drug metabolism defects
CC   (adverse drug reactions) resulting from mutations in the CYP2D6 gene, in
CC   high throughput clinical genotyping applications. The method is a novel
CC   and a multiplex method for detecting multiple mutations located in the
CC   gene encoding CYP2D6. The present sequence represents the Human CYP2d6
CC   gene which islocated in chromosome 22q13.1. NOTE: It is not possible to
CC   determine the position of the SNPs within this gene since the authors
CC   reference the positions to the ATG start codon (e.g. -1584) without
CC   indicating where the start codon is within the present sequence.
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 15;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 84
ACA61302
ID   ACA61302 standard; DNA; 9433 BP.
XX
AC   ACA61302;
XX
DT   16-JUL-2003  (first entry)
XX
DE   Human cytochrome p450 gene CYP2D6, variant sequence.
XX
KW   Human; ds; gene; cytochrome P450; CYP2D6; chromosome 22; SNP;
KW   single nucleotide polymorphism; drug metabolism; cardiovascular disorder;
KW   psychiatric disorder; drug sensitivity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(226. .227,ATT)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(971,G)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1111,T)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1726,C)
FT                   /*tag=  d
```

```
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1846,A)
FT                   /*tag= f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1846,G)
FT                   /*tag= e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(2064,A)
FT                   /*tag= g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3023,A)
FT                   /*tag= h
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5799,G)
FT                   /*tag= i
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5816. .5817,C)
FT                   /*tag= j
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1281755-A2.
XX
PD   05-FEB-2003.
XX
PF   16-JUL-2002; 2002EP-00254972.
XX
PR   31-JUL-2001; 2001US-0309111P.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Milos PM,  Webb SM;
XX
DR   WPI; 2003-373769/36.
XX
PT   New cytochrome P450 2D6 gene variants and polypeptides, useful for
PT   determining if a subject has or is at risk of developing a drug
PT   sensitivity condition or disorder that is associated with an aberrant
PT   CYP2D6 activity.
XX
PS   Claim 3; Fig 3; 88pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising a cytochrome
CC   P450 2D6 gene variant, e.g. G5799C or C5816AT (referring to the genomic
CC   sequence or the same variant nucleotide in the corresponding cDNA
CC   sequences). Also included are probes, primers (allele specific
CC   oligonucleotides) and arrays used to detect and or amplify the CYP2D6
CC   gene polymorphic regions, the variant polypeptides, antibodies which are
CC   capable of distinguishing between the variant and wild-type polypeptides,
CC   determining whether a subject has a genetic deficiency for metabolising a
CC   drug, evaluating therapy with a drug metabolised by P450 CYP2D6 and
CC   determining whether an individual is susceptible to being a poor
CC   metaboliser of drugs. The DNA probe is useful for hybrisiding to a
CC   variant form of the CYP2D6 gene. The primer is useful for amplifying the
CC   C5816TA allelic variant. The allele specific nucleotide is useful for the
CC   detection of the C5816TA allelic variant. The methods are useful for
CC   determining whether a subject has a genetic deficiency for metabolising a
CC   drug, evaluating therapy with a drug metabolised by P450 CYP2D6, and
CC   determining if an individual is susceptible to being a poor metaboliser
CC   of drugs. The nucleic acids are useful as probes or primers for
CC   determining whether a subject has a genetic deficiency for metabolising
CC   drugs that are substrates of P450 CYP2D6. The methods are useful for
CC   determining if a subject has or is at risk of developing a drug
CC   sensitivity condition or disorder that is associated with an aberrant
CC   CYP2D6 activity, e.g. an aberrant level of a CYP2D6 protein or an
CC   aberrant CYP2D6 bioactivity. The methods are also useful in selecting the
CC   appropriate drugs or determining the course of treatment to administer to
CC   a subject to treat cardiovascular or psychiatric disorders, or for
CC   treating a subject with a drug sensitivity or disorder associated with a
CC   specific allelic variant of a polymorphic region of the CYP2D6 gene. The
CC   antibodies are useful for monitoring CYP2D6 protein levels in an
CC   individual for determining whether a subject has a disease or conditions
CC   associated with an aberrant CYP2D6 protein level. The gene is located on
CC   human chromosome 22. The present sequence is the variant CYP2D6 gene
CC   carrying both the G5799C and C5816AT variations
XX
SQ   Sequence 9433 BP; 1965 A; 2647 C; 2975 G; 1846 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 10;  Length 9433;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 85
ADX00827
ID   ADX00827 standard; DNA; 9609 BP.
XX
AC   ADX00827;
XX
DT   21-APR-2005  (first entry)
XX
DE   Human CYP2D6 gene.
XX
KW   DNA purification; SNP detection; cardiovascular-gen.; hypotensive;
KW   neuroleptic; antiarrhythmic; antiemetic; analgesic; anorectic;
KW   tranquilizer; antimanic; antidepressant; allelic variant; CYP2D6 gene;
KW   diagnosis; codeine dependence; depression; hepatitis C virus infection;
KW   psychosis; schizophrenia; Parkinsons disease; forensic; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   allele          replace(4087,A)
FT                   /*tag= a
FT   allele          replace(4735,A)
FT                   /*tag= b
FT   allele          replace(4784,A)
FT                   /*tag= c
XX
PN   US2005032070-A1.
XX
PD   10-FEB-2005.
XX
PF   05-AUG-2003; 2003US-00635780.
XX
PR   05-AUG-2003; 2003US-00635780.
XX
PA   (RAIM/) RAIMUNDO S.
PA   (ZANG/) ZANGER U.
XX
PI   Raimundo S,  Zanger U;
XX
DR   WPI; 2005-161644/17.
XX
PT   Novel polynucleotide of molecular variants of Cytochrome P450 2D6
PT   (CYP2D6) gene, capable of hybridizing to CYP2D6 gene, is useful in
PT   diagnosing disease related to presence of molecular variant of CYP2D6
PT   gene.
XX
PS   Claim 1; SEQ ID NO 4; 33pp; English.
XX
CC   The invention relates to a polynucleotide (I) of molecular variants of
CC   CYP2D6 gene, chosen from polynucleotide capable of hybridizing to CYP2D6
CC   gene, where the polynucleotide consists of substitution of one or more
CC   nucleotides at position corresponding to 4784, 4735 or 4087 of the CYP2D6
CC   gene having a fully defined sequence (S1) of 9609 base pairs as given in
CC   the specification. (I) is useful for identifying a diagnostic
CC   composition, which involves (a) isolating (I) from several subgroups of
CC   individuals, where one subgroup has no prevalence for CYP2D6 associated
CC   disease, and one or more further subgroup(s) do have prevalence for a
CC   CYP2D6 associated disease, and (b) identifying a single nucleotide
CC   polymorphism by comparing the nucleic acid sequence of the polynucleotide
CC   or the gene of one subgroup having no prevalence for a CYP2D6 associated
```

CC disease, with one or more further subgroup(s) having a prevalence for a
CC CYP2D6 associated disease. (I) is useful for diagnosing a disease related
CC to the presence of a molecular variant of a CYP2D6 gene or susceptibility
CC to such a disorder, which involves determining the presence of (I) in a
CC sample from a subject. (I) is useful for diagnosing whether a subject has
CC EM, IM or PM phenotype, and for determining whether an individual is at
CC risk for a toxic reaction, non-response, insufficient response, or
CC reduced metabolic activity of CYP2D6 to treatment with a CYP2D6
CC substrate. (I) is useful in selecting a subject suffering from a CYP2D6
CC substrate treatable disease for treatment with the substrate, and in
CC treating a subject suffering from a CYP2D6 substrate treatable disease.
CC (I) is useful for detecting variant polynucleotide of CYP2D6 gene in a
CC sample, which involves contacting (I) with the sample under conditions
CC allowing interaction of variant of CYP2D6 gene with several immobilized
CC targets on (I), and determining the binding of the polynucleotide or the
CC gene to the immobilized targets on (I). (I) is useful for diagnosing a
CC disease, which involves binding of the variant polynucleotide of CYP2D6
CC gene or the gene to the immobilized targets on (IV), where the binding
CC indicates the presence or the absence of the disease or a prevalence for
CC the disease. The disease is codeine dependence, depression, hepatitis C,
CC psychosis, schizophrenia or Parkinson's disease. (I) is useful for
CC diagnosing an altered activity of the CYP2D6 enzyme, and for diagnosing a
CC polynucleotide associated with IM phenotype of CYP2D6. (I) is useful in
CC diagnosing individual's genetic constitution of the CYP2D6 status, useful
CC in personalized medicine. (I) is used for prediction of the therapeutic
CC outcome of an individual with an established drug and for avoidance of
CC side effects/toxicity due to altered activity of CYP2D6 mediated by
CC different CYP2D6 alleles. (I) is useful as forensic markers. This
CC sequence corresponds to the human CYP2D6 gene.
XX
SQ Sequence 9609 BP; 2010 A; 2696 C; 3025 G; 1878 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 14; Length 9609;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 3625 CGCATCTCCCACCCCCA 3641

RESULT 86
ADJ78567
ID ADJ78567 standard; DNA; 13278 BP.
XX
AC ADJ78567;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human cytochrome P450 isoenzyme 2D6 pseudogene SeqID5.
XX
KW primer set; variant identification; cytochrome P450 isoenzyme 2D6;
KW CYP2D6; chromosome 22q13.1; single nucleotide polymorphism; SNP;
KW low frequency variant; pharmaceutical drugs metabolism; human;
KW pseudogene; ds.
XX
OS Homo sapiens.
XX
PN WO2004009760-A2.
XX
PD 29-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021468.
XX
PR 18-JUL-2002; 2002US-0397010P.
XX
PA (BIOV-) BIOVENTURES INC.
XX
PI Dawson EP;
XX
DR WPI; 2004-132938/13.
XX
PT New primer set useful for screening a polynucleotide sample to detect and
PT identify variants in the cytochrome P450 isoenzyme 2D6 gene, and for
PT detecting low frequency variants affecting pharmaceutical drugs
PT metabolism.
XX
PS Disclosure; SEQ ID NO 5; 51pp; English.
XX
CC This invention relates to novel primer sets that can be used to screen a
CC polynucleotide sample to detect and identify variants in the cytochrome
CC P450 isoenzyme 2D6 (CYP2D6) gene. The gene is located on chromosome
CC 22q13.1 and contains several single nucleotide polymorphisms, the details
CC of which are disclosed in the specification. The methods and compositions
CC of the present invention are useful for screening a polynucleotide sample
CC to detect and identify variants in the cytochrome P450 isoenzyme 2D6 gene
CC and detecting low frequency variants affecting pharmaceutical drugs
CC metabolism. The present sequence is that of a human cytochromome p450
CC isoenzyme 2D6 pseudogene which was used during the design of the primer
CC sets of the invention to ensure specific amplification of the correct
CC gene sequence.
XX
SQ Sequence 13278 BP; 2902 A; 3664 C; 3968 G; 2744 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 13278;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||
Db 3046 CGCATCTCCCACCCCCA 3062

RESULT 87
ADM28895
ID ADM28895 standard; DNA; 13278 BP.
XX
AC ADM28895;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human pseudogene #2 located near CYP2D6 gene.
XX
KW Human; cytochrome P450 isoenzyme 2D6; CYP2D6 isoenzyme;
KW altered metabolism; chromosome 22q; ds.
XX
OS Homo sapiens.
XX
PN US2004072235-A1.
XX
PD 15-APR-2004.
XX
PF 12-NOV-2003; 2003US-00712363.
XX
PR 20-JUL-2001; 2001US-0306675P.
PR 18-JUL-2002; 2002US-00360790.
PR 09-JUL-2003; 2003WO-US021468.
XX
PA (DAWS/) DAWSON E P.
XX
PI Dawson EP;
XX
DR WPI; 2004-328568/30.
XX
PT Novel primer set for screening a polynucleotide sample to detect and
PT identify variants in the cytochrome P450 isoenzyme 2D6 (CYP2D6) gene in a
PT polynucleotide sample or a population.
XX
PS Disclosure; SEQ ID NO 5; 47pp; English.
XX
CC The present invention relates to a primer set that can be used to screen
CC a polynucleotide sample to detect and identify variants in the human
CC cytochrome P450 isoenzyme 2D6 (CYP2D6) gene. Also disclosed is a kit for
CC the above screening method, a method for predicting the potential for
CC altered metabolism of a substance, including one or more than one
CC pharmaceutical drug, by a first individual compared to a second control

CC individual, where the substance is metabolised by the CYP2D6 isoenzyme, a
CC purified or isolated variant of wild-type CYP2D6 isoenzyme having one or
CC more than one of the alterations chosen from F-I at position 120, F-F at
CC position 120, E-K at position 155, R-R at position 194, F-F at position
CC 219, L-L at position 276, H-H at position 324, R-STOP at position 344, Y-
CC C at position 355, H-H at position 361, V-FRAMESHIFT at position 363, E-K
CC at position 418, H-Y at position 478 and F-F at position 483. The primer
CC set is useful for screening a polynucleotide sample to detect and
CC identify the presence of one or more than one variant in the CYP2D6 gene
CC in the sample. The primer set permits amplification from a small
CC polynucleotide sample of selected portions of the coding portion of the
CC CYP2D6 gene, or amplification of the entire coding portion of CYP2D6, as
CC well as the flanking intronic sequences that are relevant to recognition
CC of splice sites. The primer set further permits the detection of genetic
CC variants of CYP2D6 without interference from pseudogenes or from
CC homologous or paralogous genes of non-CYP2D6 cytochrome p450 genes. The
CC primer set also permits the detection of low frequency variants that
CC affect pharmaceutical drugs metabolism, thereby decreasing the false
CC negative rate in variant screening. The present sequence represents a
CC human pseudogene located on chromosome 22q near the CYP2D6 gene.
XX
SQ Sequence 13278 BP; 2902 A; 3664 C; 3968 G; 2744 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 13278;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
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Db 3046 CGCATCTCCCACCCCCA 3062

RESULT 88
ADJ78568
ID ADJ78568 standard; DNA; 13677 BP.
XX
AC ADJ78568;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human cytochrome P450 isoenzyme 2D6 pseudogene SeqID6.
XX
KW primer set; variant identification; cytochrome P450 isoenzyme 2D6;
KW CYP2D6; chromosome 22q13.1; single nucleotide polymorphism; SNP;
KW low frequency variant; pharmaceutical drugs metabolism; human;
KW pseudogene; ds.
XX
OS Homo sapiens.
XX
PN WO2004009760-A2.
XX
PD 29-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021468.
XX
PR 18-JUL-2002; 2002US-0397010P.
XX
PA (BIOV-) BIOVENTURES INC.
XX
PI Dawson EP;
XX
DR WPI; 2004-132938/13.
XX
PT New primer set useful for screening a polynucleotide sample to detect and
PT identify variants in the cytochrome P450 isoenzyme 2D6 gene, and for
PT detecting low frequency variants affecting pharmaceutical drugs
PT metabolism.
XX
PS Disclosure; SEQ ID NO 6; 51pp; English.
XX
CC This invention relates to novel primer sets that can be used to screen a
CC polynucleotide sample to detect and identify variants in the cytochrome
CC P450 isoenzyme 2D6 (CYP2D6) gene. The gene is located on chromosome
CC 22q13.1 and contains several single nucleotide polymorphisms, the details
CC of which are disclosed in the specification. The methods and compositions
CC of the present invention are useful for screening a polynucleotide sample
CC to detect and identify variants in the cytochrome P450 isoenzyme 2D6 gene
CC and detecting low frequency variants affecting pharmaceutical drugs
CC metabolism. The present sequence is that of a human cytochromome p450
CC isoenzyme 2D6 pseudogene which was used during the design of the primer
CC sets of the invention to ensure specific amplification of the correct
CC gene sequence.
XX
SQ Sequence 13677 BP; 3066 A; 3775 C; 4107 G; 2729 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 12; Length 13677;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
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Db 3426 CGCATCTCCCACCCCCA 3442

RESULT 89
ADM28896
ID ADM28896 standard; DNA; 13677 BP.
XX
AC ADM28896;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human pseudogene #3 located near CYP2D6 gene.
XX
KW Human; cytochrome P450 isoenzyme 2D6; CYP2D6 isoenzyme;
KW altered metabolism; chromosome 22q; ds.
XX
OS Homo sapiens.
XX
PN US2004072235-A1.
XX
PD 15-APR-2004.
XX
PF 12-NOV-2003; 2003US-00712363.
XX
PR 20-JUL-2001; 2001US-0306675P.
PR 18-JUL-2002; 2002US-00360790.
PR 09-JUL-2003; 2003WO-US021468.
XX
PA (DAWS/) DAWSON E P.
XX
PI Dawson EP;
XX
DR WPI; 2004-328568/30.
XX
PT Novel primer set for screening a polynucleotide sample to detect and
PT identify variants in the cytochrome P450 isoenzyme 2D6 (CYP2D6) gene in a
PT polynucleotide sample or a population.
XX
PS Disclosure; SEQ ID NO 6; 47pp; English.
XX
CC The present invention relates to a primer set that can be used to screen
CC a polynucleotide sample to detect and identify variants in the human
CC cytochrome P450 isoenzyme 2D6 (CYP2D6) gene. Also disclosed is a kit for
CC the above screening method, a method for predicting the potential for
CC altered metabolism of a substance, including one or more than one
CC pharmaceutical drug, by a first individual compared to a second control
CC individual, where the substance is metabolised by the CYP2D6 isoenzyme, a
CC purified or isolated variant of wild-type CYP2D6 isoenzyme having one or
CC more than one of the alterations chosen from F-I at position 120, F-F at
CC position 120, E-K at position 155, R-R at position 194, F-F at position
CC 219, L-L at position 276, H-H at position 324, R-STOP at position 344, Y-
CC C at position 355, H-H at position 361, V-FRAMESHIFT at position 363, E-K
CC at position 418, H-Y at position 478 and F-F at position 483. The primer
CC set is useful for screening a polynucleotide sample to detect and
CC identify the presence of one or more than one variant in the CYP2D6 gene

```
CC   in the sample. The primer set permits amplification from a small
CC   polynucleotide sample of selected portions of the coding portion of the
CC   CYP2D6 gene, or amplification of the entire coding portion of CYP2D6, as
CC   well as the flanking intronic sequences that are relevant to recognition
CC   of splice sites. The primer set further permits the detection of genetic
CC   variants of CYP2D6 without interference from pseudogenes or from
CC   homologous or paralogous genes of non-CYP2D6 cytochrome p450 genes. The
CC   primer set also permits the detection of low frequency variants that
CC   affect pharmaceutical drugs metabolism, thereby decreasing the false
CC   negative rate in variant screening. The present sequence represents a
CC   human pseudogene located on chromosome 22q near the CYP2D6 gene.
XX
SQ   Sequence 13677 BP; 3066 A; 3775 C; 4107 G; 2729 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 13677;
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3426 CGCATCTCCCACCCCCA 3442


RESULT 90
ADJ78566
ID   ADJ78566 standard; DNA; 17060 BP.
XX
AC   ADJ78566;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human cytochrome P450 isoenzyme 2D6 pseudogene SeqID4.
XX
KW   primer set; variant identification; cytochrome P450 isoenzyme 2D6;
KW   CYP2D6; chromosome 22q13.1; single nucleotide polymorphism; SNP;
KW   low frequency variant; pharmaceutical drugs metabolism; human;
KW   pseudogene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004009760-A2.
XX
PD   29-JAN-2004.
XX
PF   09-JUL-2003; 2003WO-US021468.
XX
PR   18-JUL-2002; 2002US-0397010P.
XX
PA   (BIOV-) BIOVENTURES INC.
XX
PI   Dawson EP;
XX
DR   WPI; 2004-132938/13.
XX
PT   New primer set useful for screening a polynucleotide sample to detect and
PT   identify variants in the cytochrome P450 isoenzyme 2D6 gene, and for
PT   detecting low frequency variants affecting pharmaceutical drugs
PT   metabolism.
XX
PS   Disclosure; SEQ ID NO 4; 51pp; English.
XX
CC   This invention relates to novel primer sets that can be used to screen a
CC   polynucleotide sample to detect and identify variants in the cytochrome
CC   P450 isoenzyme 2D6 (CYP2D6) gene. The gene is located on chromosome
CC   22q13.1 and contains several single nucleotide polymorphisms, the details
CC   of which are disclosed in the specification. The methods and compositions
CC   of the present invention are useful for screening a polynucleotide sample
CC   to detect and identify variants in the cytochrome P450 isoenzyme 2D6 gene
CC   and detecting low frequency variants affecting pharmaceutical drugs
CC   metabolism. The present sequence is that of a human cytochromome p450
CC   isoenzyme 2D6 pseudogene which was used during the design of the primer
CC   sets of the invention to ensure specific amplification of the correct
CC   gene sequence.
XX
SQ   Sequence 17060 BP; 3517 A; 4595 C; 5034 G; 3914 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 17060;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db      13129 CGCATCTCCCACCCCCA 13145


RESULT 91
ADM28894
ID   ADM28894 standard; DNA; 17060 BP.
XX
AC   ADM28894;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human pseudogene #1 located near CYP2D6 gene.
XX
KW   Human; cytochrome P450 isoenzyme 2D6; CYP2D6 isoenzyme;
KW   altered metabolism; chromosome 22q; ds.
XX
OS   Homo sapiens.
XX
PN   US2004072235-A1.
XX
PD   15-APR-2004.
XX
PF   12-NOV-2003; 2003US-00712363.
XX
PR   20-JUL-2001; 2001US-0306675P.
PR   18-JUL-2002; 2002US-00360790.
PR   09-JUL-2003; 2003WO-US021468.
XX
PA   (DAWS/) DAWSON E P.
XX
PI   Dawson EP;
XX
DR   WPI; 2004-328568/30.
XX
PT   Novel primer set for screening a polynucleotide sample to detect and
PT   identify variants in the cytochrome P450 isoenzyme 2D6 (CYP2D6) gene in a
PT   polynucleotide sample or a population.
XX
PS   Disclosure; SEQ ID NO 4; 47pp; English.
XX
CC   The present invention relates to a primer set that can be used to screen
CC   a polynucleotide sample to detect and identify variants in the human
CC   cytochrome P450 isoenzyme 2D6 (CYP2D6) gene. Also disclosed is a kit for
CC   the above screening method, a method for predicting the potential for
CC   altered metabolism of a substance, including one or more than one
CC   pharmaceutical drug, by a first individual compared to a second control
CC   individual, where the substance is metabolised by the CYP2D6 isoenzyme, a
CC   purified or isolated variant of wild-type CYP2D6 isoenzyme having one or
CC   more than one of the alterations chosen from F-I at position 120, F-F at
CC   position 120, E-K at position 155, R-R at position 194, F-F at position
CC   219, L-L at position 276, H-H at position 324, R-STOP at position 344, Y-
CC   C at position 355, H-H at position 361, V-FRAMESHIFT at position 363, E-K
CC   at position 418, H-Y at position 478 and F-F at position 483. The primer
CC   set is useful for screening a polynucleotide sample to detect and
CC   identify the presence of one or more than one variant in the CYP2D6 gene
CC   in the sample. The primer set permits amplification from a small
CC   polynucleotide sample of selected portions of the coding portion of the
CC   CYP2D6 gene, or amplification of the entire coding portion of CYP2D6, as
CC   well as the flanking intronic sequences that are relevant to recognition
CC   of splice sites. The primer set further permits the detection of genetic
CC   variants of CYP2D6 without interference from pseudogenes or from
CC   homologous or paralogous genes of non-CYP2D6 cytochrome p450 genes. The
CC   primer set also permits the detection of low frequency variants that
CC   affect pharmaceutical drugs metabolism, thereby decreasing the false
```

```
CC   negative rate in variant screening. The present sequence represents a
CC   human pseudogene located on chromosome 22q near the CYP2D6 gene.
XX
SQ   Sequence 17060 BP; 3516 A; 4595 C; 5034 G; 3915 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 12;  Length 17060;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db      13129 CGCATCTCCCACCCCCA 13145


RESULT 92
AEF35808
ID   AEF35808 standard; DNA; 18000 BP.
XX
AC   AEF35808;
XX
DT   23-MAR-2006  (first entry)
XX
DE   Human cytochrome P450 2D6 DNA neighboring loci.
XX
KW   diagnosis; prophylaxis; hepatitis B infection; hepatitis C infection;
KW   hepatitis D infection; drug-induced hepatotoxicity; liver tumor;
KW   liver cirrhosis; fibrosis; autoimmune hepatitis;
KW   primary biliary cirrhosis; primary sclerosing cholangitis;
KW   hemochromatosis; Wilson's disease; alpha-1 antitrypsin deficiency;
KW   celiac disease; amyloidosis; gastrointestinal disease;
KW   metabolic disorder; inflammation; cardiant; antiinflammatory;
KW   hepatotropic; virucide; gastrointestinal-gen.; cns-gen.; metabolic;
KW   immunosuppressive; cytostatic; cytochrome P450 2D6; CYP2D6; ds.
XX
OS   Homo sapiens.
XX
PN   WO2006003654-A2.
XX
PD   12-JAN-2006.
XX
PF   30-JUN-2005; 2005WO-IL000700.
XX
PR   01-JUL-2004; 2004US-0584179P.
XX
PA   (MEDI-) MEDICAL RES FUND TEL AVIV SOURASKY MED.
XX
PI   Oren R;
XX
DR   WPI; 2006-090428/09.
XX
PT   Determining if an individual is predisposed to fast progression of liver
PT   fibrosis comprises determining a presence or absence of at least one fast
PT   progression liver fibrosis-associated genotype.
XX
PS   Claim 7; SEQ ID NO 10; 105pp; English.
XX
CC   The invention relates to a method of determining if an individual is
CC   predisposed to fast progression of liver fibrosis or liver cirrhosis
CC   comprising determining a presence or absence, in a homozygous or
CC   heterozygous form, of at least one fast progression liver fibrosis-
CC   associated genotype in the CYP2D6, CYP3A5, CYP2E1, or APO E locus or in
CC   neighboring loci of the individual, where the neighboring loci is in
CC   linkage disequilibrium with the locus, thus determining if the individual
CC   is predisposed to fast progression of liver fibrosis; a kit to carry out
CC   the method; a method of preventing fast progression of liver fibrosis in
CC   an individual, by upregulating CYP2D6 expression and/or activity; and a
CC   method of determining if a drug molecule is capable of inducing or
CC   accelerating development of fast progression of liver fibrosis in an
CC   individual. The individual is suffering from a hepatitis viral infection
CC   caused by hepatitis B, C or D virus, a hepatotoxicity (alcohol- or drug-
CC   induced), a liver cancer, a non-alcoholic fatty liver disease (NAFLD), an
CC   autoimmune disease (autoimmune hepatitis (AIH), primary biliary cirrhosis
CC   (PBC), or primary sclerosing cholangitis (PSC)), a metabolic liver
CC   disease (Hemochromatosis, Wilson's disease, or alpha 1 anti trypsin), or
CC   a disease with secondary involvement of the liver (celiac disease and/or
CC   amyloidosis). The method and kit are useful for determining if an
CC   individual is predisposed to fast progression of liver fibrosis. The
CC   method and drug are useful for preventing liver cirrhosis and fast
CC   progression of liver fibrosis. This sequence is human cytochrome P450 2D6
CC   DNA neighboring loci.
XX
SQ   Sequence 18000 BP; 4213 A; 4884 C; 5192 G; 3711 T; 0 U; 0 Other;

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  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||
Db       9555 CGCATCTCCCACCCCCA 9571


Search completed: July  3, 2006, 06:18:57
Job time : 290 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:13:35 ; Search time 2295 Seconds
(without alignments)
414.217 Million cell updates/sec

Title: US-10-615-497-9
Perfect score: 17
Sequence: 1 cgcatctcccacccccca 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	6	16	94.1	328	1	AA164102	AA164102 mr23g08.r
	7	16	94.1	337	3	BM931322	BM931322 UI-E-EJ1-
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	11	16	94.1	478	14	DE270506	DE270506 Oryzias l
	12	16	94.1	480	12	CE711263	CE711263 tigr-gss-
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c	14	16	94.1	589	1	AI875666	AI875666 uk51b12.x
	15	16	94.1	619	12	CE192695	CE192695 tigr-gss-
	16	16	94.1	661	3	BU058943	BU058943 UI-M-FR0-
	17	16	94.1	675	8	CV560308	CV560308 UI-M-HA0-
	18	16	94.1	684	12	CC770850	CC770850 CH240_5L6
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	20	16	94.1	712	5	CD806745	CD806745 UI-M-GW0-
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	22	16	94.1	756	5	CD806736	CD806736 UI-M-GW0-
	23	16	94.1	757	5	CD806725	CD806725 UI-M-GW0-
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	25	16	94.1	831	14	CT143069	CT143069 Sus scrof
	26	16	94.1	838	14	AG495800	AG495800 Mus muscu
	27	16	94.1	840	12	CC508980	CC508980 CH240_351
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c	29	16	94.1	849	9	DN072595	DN072595 JGI_CABD7
c	30	16	94.1	850	10	DT530095	DT530095 JGI_CABH3
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ALIGNMENTS

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DEFINITION OP__Ba0003F17.r OP__Ba Oryza punctata genomic clone OP__Ba0003F17 3', genomic survey sequence.
ACCESSION CW507956
VERSION CW507956.1 GI:53837461
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 632)
AUTHORS SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
TITLE OMAP Project - Purdue University
JOURNAL Unpublished (2004)
COMMENT Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lucy version 1.19s. Bases 205-836 of the raw sequence (length 1396) were retained after clipping.
PCR PRimers
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BACKWARD: CAC TCA TTA GGC ACC CCA
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Plate: 0003 row: F column: 17
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Class: BAC ends.
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/db_xref="taxon:4537"

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                     /tissue_type="young leaves"
                     /lab_host="DH10B-T1 phage resistant"
                     /clone_lib="OP__Ba"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 13;  Length 632;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        523 CGCATCTCCCACCCCCA 507


RESULT 2
CL672428/c
LOCUS       CL672428                731 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI016d_E03 - PRI016d.B21 (731) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL672428
VERSION     CL672428.1  GI:50172706
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
   PUBMED   14681447
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 13;  Length 731;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        728 CGCATCTCCCACCCCCA 712


RESULT 3
CR896623/c
LOCUS       CR896623                732 bp    DNA     linear   GSS 23-NOV-2004
DEFINITION  Sus scrofa BES, genomic survey sequence.
ACCESSION   CR896623
VERSION     CR896623.1  GI:56221120
KEYWORDS    GSS; Bac-end sequence BES; Genome Survey Sequence.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
            Chardon,P.
  TITLE     Construction of a swine BAC library: application to the
            characterization and mapping of porcine type C endoviral elements
  JOURNAL   Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
   PUBMED   10449899
REFERENCE   2  (bases 1 to 732)
  AUTHORS   Chardon,P., Iannuccelli,N., Roig,A., Dossat,C., Demars,J.,
            Rogel-Gaillard,C., Roy,A., Schibler,L. and Milan,D.
  TITLE     A physical map of the swine genome
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 732)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /strain="Large White"
                     /db_xref="taxon:9823"
                     /clone="bI0230A05"
                     /sex="male"
                     /cell_type="fibroblast"
                     /clone_lib="SBAB"
                     /note="Genoscope sequence ID : IH0AAA22CC04FM1"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 14;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        154 CGCATCTCCCACCCCCA 138


RESULT 4
BB898440/c
LOCUS       BB898440                1357 bp    mRNA    linear   EST 09-SEP-2005
DEFINITION  BB898440 Sugano cDNA library, adult liver Macaca fascicularis cDNA
            clone Q1v-U239A-F1 3', mRNA sequence.
ACCESSION   BB898440
VERSION     BB898440.1  GI:74351779
KEYWORDS    EST.
SOURCE      Macaca fascicularis (crab-eating macaque)
  ORGANISM  Macaca fascicularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1357)
  AUTHORS   Uno,Y., Suzuki,Y., Osada,N., Hashimoto,K., Aburatani,H., Sugano,S.
            and Inoue,I.
  TITLE     Analyses of Macaque cDNAs
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: ysuzuki@hgc.jp.
FEATURES             Location/Qualifiers
     source          1. .1357
                     /organism="Macaca fascicularis"
```

```
                     /mol_type="mRNA"
                     /db_xref="taxon:9541"
                     /clone="Qlv-U239A-F1"
                     /tissue_type="adult liver"
                     /clone_lib="Sugano cDNA library, adult liver"
ORIGIN

  Query Match             100.0%;  Score 17;  DB 7;  Length 1357;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        522 CGCATCTCCCACCCCCA 506


RESULT 5
CA567279
LOCUS       CA567279                244 bp    mRNA    linear   EST 19-NOV-2002
DEFINITION  K0412C02-5N NIA Mouse Mesenchymal Stem Cell cDNA Library (Long) Mus
            musculus cDNA clone NIA:K0412C02 IMAGE:30060217 5', mRNA sequence.
ACCESSION   CA567279
VERSION     CA567279.1  GI:25111952
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 244)
  AUTHORS   Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G.,
            Umezawa,A. and Ko,M.S.H.
  TITLE     Systematic Analyses of NIA Mouse Mesenchymal Stem Cell cDNA Library
            (Long)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: K0412  row: C  column: 02
            Seq primer: M13 Reverse
            High quality sequence stop: 244
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .244
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C3H/He"
                     /db_xref="niaEST:K0412C02-5N"
                     /db_xref="taxon:10090"
                     /clone="NIA:K0412C02 IMAGE:30060217"
                     /tissue_type="Mesenchymal stem cell"
                     /cell_line="9-15-C cells"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Mesenchymal Stem Cell cDNA Library
                     (Long)"
                     /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
                     NotI; Mouse cDNA project by the Laboratory of Genetics,
                     National Institute on Aging (NIA), Intramural Research
                     Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
                     a long-transcript enriched cDNA library (Ref. Genome Res.
                     11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
                     obtained from Dr. Akihiro Umezawa (Keio University School
                     of Medicine, Japan). Double-stranded cDNAs were
                     synthesized with an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                     2.2 ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pSPORT1 plasmid vector.
                     The DH10B E. coli host was transformed with the ligation
                     mixture by the standard chemical method. The average
                     insert size is about 2.5 kb. The library was constructed
                     by Yulan Piao (NIA)."
ORIGIN

  Query Match             94.1%;  Score 16;  DB 4;  Length 244;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCC 16
              ||||||||||||||||
Db          2 CGCATCTCCCACCCCC 17


RESULT 6
AA164102
LOCUS       AA164102                328 bp    mRNA    linear   EST 16-FEB-1997
DEFINITION  mr23g08.r1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:598334
            5', mRNA sequence.
ACCESSION   AA164102
VERSION     AA164102.1  GI:1740065
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 328)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:363766
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 321.
FEATURES             Location/Qualifiers
     source          1. .328
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:598334"
                     /sex="male"
                     /tissue_type="Spleen"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares mouse 3NbMS"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through
                     three rounds of normalization, and was constructed by
                     Bento Soares and M.Fatima Bonaldo."
```

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ORIGIN

  Query Match             94.1%;  Score 16;  DB 1;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCCA 17
              ||||||||||||||||
Db        117 GCATCTCCCACCCCCA 132


RESULT 7
BM931322
LOCUS       BM931322                337 bp    mRNA    linear   EST 13-MAR-2002
DEFINITION  UI-E-EJ1-ajj-h-22-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-ajj-h-22-0-UI 5', mRNA sequence.
ACCESSION   BM931322
VERSION     BM931322.1  GI:19390495
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 337)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 REVERSE.
FEATURES             Location/Qualifiers
     source          1. .337
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJ1-ajj-h-22-0-UI"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EJ1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes,
                     AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
                     AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
                     Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
                     library was created for the program, Gene Discovery in the
                     Visual System, supported by National Eye Institute (NEI)."

ORIGIN

  Query Match             94.1%;  Score 16;  DB 3;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCC 16
              ||||||||||||||||
Db         90 CGCATCTCCCACCCCC 105


RESULT 8
BF893184/c
LOCUS       BF893184                358 bp    mRNA    linear   EST 18-JAN-2001
DEFINITION  PM1-MT0143-101100-003-g02 MT0143 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF893184
VERSION     BF893184.1  GI:12284643
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-MT0143-
            101100-003-g02&t3=2000-11-10&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 357.
FEATURES             Location/Qualifiers
     source          1. .358
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="MT0143"
                     /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

  Query Match             94.1%;  Score 16;  DB 2;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCCA 17
              ||||||||||||||||
Db        211 GCATCTCCCACCCCCA 196
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RESULT 9
AJ791138/c
LOCUS       AJ791138                443 bp    mRNA    linear   EST 08-DEC-2004
DEFINITION  AJ791138 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
            018_2_07_n16, mRNA sequence.
ACCESSION   AJ791138
VERSION     AJ791138.1  GI:51061222
KEYWORDS    EST.
SOURCE      Antirrhinum majus (snapdragon)
  ORGANISM  Antirrhinum majus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
            Antirrhinum.
REFERENCE   1  (bases 1 to 443)
  AUTHORS   Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
            Saedler,H. and Zachgo,S.
  TITLE     Characterization of Antirrhinum Petal Development and
            Identification of Target Genes of the Class B MADS Box Gene
            DEFICIENS
  JOURNAL   Plant Cell 16 (12), 3197-3215 (2004)
   PUBMED   15539471
COMMENT     Contact: Schwarz-Sommer Z
            Molekulare Pflanzengenetik
            MPI fuer Zuechtungsforschung
            Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES             Location/Qualifiers
     source          1. .443
                     /organism="Antirrhinum majus"
                     /mol_type="mRNA"
                     /db_xref="taxon:4151"
                     /clone="018_2_07_n16"
                     /tissue_type="whole plant"
                     /clone_lib="Antirrhinum majus whole plant"
ORIGIN

  Query Match             94.1%;  Score 16;  DB 1;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCCA 17
              ||||||||||||||||
Db        239 GCATCTCCCACCCCCA 224


RESULT 10
AZ771494/c
LOCUS       AZ771494                474 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0573L12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0573L12 R, genomic survey sequence.
ACCESSION   AZ771494
VERSION     AZ771494.1  GI:12893815
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 474)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0573  row: L  column: 12
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 474.
FEATURES             Location/Qualifiers
     source          1. .474
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0573L12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             94.1%;  Score 16;  DB 11;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCC 16
              ||||||||||||||||
Db         50 CGCATCTCCCACCCCC 35


RESULT 11
DE270506
LOCUS       DE270506                478 bp    DNA     linear   GSS 22-SEP-2005
DEFINITION  Oryzias latipes DNA, clone: ola1-194P24.F, genomic survey sequence.
ACCESSION   DE270506
VERSION     DE270506.1  GI:76063334
KEYWORDS    GSS.
SOURCE      Oryzias latipes (Japanese medaka)
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1
  AUTHORS   Fujiyama,A., Toyoda,A., Kuroki,Y. and Sakaki,Y.
  TITLE     BAC end sequences of Ola1 Oryzias latipes Library
  JOURNAL   Published Only in Database (2005)
REFERENCE   2  (bases 1 to 478)
  AUTHORS   Fujiyama,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-2005) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:afujiyam@gsc.riken.jp, URL:http://stt.gsc.riken.jp/,
            Tel:81-3-4212-2558, Fax:81-3-3556-1916)
COMMENT     This work was done in collaboration with Takeda, H. (1), Naruse, K.
```

```
            (2)
            and Narita, T. (3)
            (1) Department of Biological Science,
            University of Tokyo
            Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, JAPAN
            Phone: +81-3-5841-4431
            Fax: +81-3-5841-4993
            E-mail: htakeda.s.u-tokyo.ac.jp
            (2) Department of Biological Science,
            University of Tokyo
            Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, JAPAN
            Phone: +81-3-5841-4431
            Fax: +81-3-5841-4993
            E-mail: naruse.s.u-tokyo.ac.jp
            (3) Department of Biological Science,
            University of Tokyo
            Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, JAPAN
            Phone: +81-3-5841-4431
            Fax: +81-3-5841-4993
            E-mail: tanarita.s.u-tokyo.ac.jp
            PRIMERS
                 Sequencing : Forward
            LIBRARY
                 Vector     : pKS145
                 R.Site 1   : SacI
                 L.Site 2   : SacI.
FEATURES             Location/Qualifiers
     source          1. .478
                     /organism="Oryzias latipes"
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                     /clone_lib="BAC end sequences of Ola1 Oryzias latipes
                     library"
ORIGIN

  Query Match             94.1%;  Score 16;  DB 14;  Length 478;
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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCCA 17
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Db        340 GCATCTCCCACCCCCA 355


RESULT 12
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LOCUS       CE711263                480 bp    DNA     linear   GSS 29-SEP-2003
DEFINITION  tigr-gss-dog-17000369470306 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE711263
VERSION     CE711263.1  GI:37030701
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
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                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             94.1%;  Score 16;  DB 12;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCCA 17
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Db        423 GCATCTCCCACCCCCA 438


RESULT 13
AI647634/c
LOCUS       AI647634                584 bp    mRNA    linear   EST 30-APR-1999
DEFINITION  uk36b05.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
            IMAGE:1971057 3', mRNA sequence.
ACCESSION   AI647634
VERSION     AI647634.1  GI:4726312
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:987797
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end
            Seq primer: custom primer used
            High quality sequence stop: 515.
FEATURES             Location/Qualifiers
     source          1. .584
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                     /strain="C57BL"
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                     /clone="IMAGE:1971057"
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                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse kidney mkia"
                     /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
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vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

ORIGIN

Query Match 94.1%; Score 16; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CGCATCTCCCACCCCC 16
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Db        471 CGCATCTCCCACCCCC 456
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RESULT 14
AI875666/c
LOCUS AI875666 589 bp mRNA linear EST 21-JUL-1999
DEFINITION uk51b12.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1972511 3', mRNA sequence.
ACCESSION AI875666
VERSION AI875666.1 GI:5549715
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 589)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: uk51b12.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:989251
Seq primer: custom primer used
High quality sequence stop: 502.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
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/clone="IMAGE:1972511"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

ORIGIN

Query Match 94.1%; Score 16; DB 1; Length 589;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CGCATCTCCCACCCCC 16
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Db        475 CGCATCTCCCACCCCC 460
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RESULT 15
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LOCUS CE192695 619 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000371473247 Dog Library Canis familiaris genomic, genomic survey sequence.
ACCESSION CE192695
VERSION CE192695.1 GI:35348348
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 619)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES Location/Qualifiers
source 1. .619
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 94.1%; Score 16; DB 12; Length 619;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 GCATCTCCCACCCCCA 17
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Job time : 2298 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: July 3, 2006, 06:14:27 ; Search time 698 Seconds
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Title: US-10-615-497-9
Perfect score: 17
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 67

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Post-processing: Minimum Match 100%
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	100.0	17	8	US-10-615-497-9	Sequence 9, Appli
2	17	100.0	24	7	US-10-411-954-36	Sequence 36, Appl
3	17	100.0	24	8	US-10-617-070-36	Sequence 36, Appl
4	17	100.0	24	10	US-10-956-507-36	Sequence 36, Appl
5	17	100.0	25	7	US-10-411-954-66	Sequence 66, Appl
6	17	100.0	25	7	US-10-411-954-288	Sequence 288, App
7	17	100.0	25	8	US-10-617-070-66	Sequence 66, Appl
8	17	100.0	25	8	US-10-617-070-288	Sequence 288, App
9	17	100.0	25	8	US-10-617-070-368	Sequence 368, App
10	17	100.0	25	10	US-10-956-507-66	Sequence 66, Appl
11	17	100.0	25	10	US-10-956-507-288	Sequence 288, App
12	17	100.0	25	10	US-10-956-507-368	Sequence 368, App
13	17	100.0	42	7	US-10-411-954-252	Sequence 252, App
14	17	100.0	42	7	US-10-411-954-253	Sequence 253, App
15	17	100.0	42	8	US-10-617-070-252	Sequence 252, App
16	17	100.0	42	8	US-10-617-070-253	Sequence 253, App
17	17	100.0	42	10	US-10-956-507-252	Sequence 252, App
18	17	100.0	42	10	US-10-956-507-253	Sequence 253, App
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c 20	17	100.0	43	7	US-10-411-954-40	Sequence 40, Appl
c 21	17	100.0	43	8	US-10-617-070-39	Sequence 39, Appl
c 22	17	100.0	43	8	US-10-617-070-40	Sequence 40, Appl
c 23	17	100.0	43	10	US-10-956-507-39	Sequence 39, Appl
c 24	17	100.0	43	10	US-10-956-507-40	Sequence 40, Appl
c 25	17	100.0	44	7	US-10-411-954-69	Sequence 69, Appl
c 26	17	100.0	44	7	US-10-411-954-70	Sequence 70, Appl
c 27	17	100.0	44	7	US-10-411-954-291	Sequence 291, App
c 28	17	100.0	44	7	US-10-411-954-292	Sequence 292, App
c 29	17	100.0	44	8	US-10-617-070-69	Sequence 69, Appl
c 30	17	100.0	44	8	US-10-617-070-70	Sequence 70, Appl
c 31	17	100.0	44	8	US-10-617-070-291	Sequence 291, App
c 32	17	100.0	44	8	US-10-617-070-292	Sequence 292, App
c 33	17	100.0	44	8	US-10-617-070-371	Sequence 371, App
c 34	17	100.0	44	8	US-10-617-070-372	Sequence 372, App
c 35	17	100.0	44	10	US-10-956-507-69	Sequence 69, Appl
c 36	17	100.0	44	10	US-10-956-507-70	Sequence 70, Appl
c 37	17	100.0	44	10	US-10-956-507-291	Sequence 291, App
c 38	17	100.0	44	10	US-10-956-507-292	Sequence 292, App
c 39	17	100.0	44	10	US-10-956-507-371	Sequence 371, App
c 40	17	100.0	44	10	US-10-956-507-372	Sequence 372, App
41	17	100.0	51	3	US-09-880-732-20	Sequence 20, Appl
42	17	100.0	51	3	US-09-880-732-21	Sequence 21, Appl
43	17	100.0	121	7	US-10-260-638-101	Sequence 101, App
c 44	17	100.0	121	7	US-10-260-638-102	Sequence 102, App
45	17	100.0	490	7	US-10-156-995-79	Sequence 79, Appl
46	17	100.0	490	7	US-10-188-359-201	Sequence 201, App
47	17	100.0	663	6	US-10-027-632-150088	Sequence 150088,
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51	17	100.0	900	7	US-10-165-410A-18	Sequence 18, Appl
c 52	17	100.0	995	12	US-10-301-480-600536	Sequence 600536,
c 53	17	100.0	995	12	US-10-301-480-1213945	Sequence 1213945,
54	17	100.0	1190	7	US-10-156-995-75	Sequence 75, Appl
55	17	100.0	1190	7	US-10-188-359-228	Sequence 228, App
56	17	100.0	1450	3	US-09-747-538-1	Sequence 1, Appli
57	17	100.0	2170	7	US-10-156-995-63	Sequence 63, Appl
58	17	100.0	2170	7	US-10-156-995-64	Sequence 64, Appl
59	17	100.0	4375	8	US-10-712-363-7	Sequence 7, Appli
60	17	100.0	9432	3	US-09-942-310-1	Sequence 1, Appli
61	17	100.0	9432	6	US-10-209-737-1	Sequence 1, Appli
62	17	100.0	9432	8	US-10-712-363-1	Sequence 1, Appli
63	17	100.0	9433	6	US-10-209-737-2	Sequence 2, Appli
64	17	100.0	9609	9	US-10-635-780-4	Sequence 4, Appli
65	17	100.0	13278	8	US-10-712-363-5	Sequence 5, Appli
66	17	100.0	13677	8	US-10-712-363-6	Sequence 6, Appli
67	17	100.0	17060	8	US-10-712-363-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-615-497-9
; Sequence 9, Application US/10615497
; Publication No. US20040091909A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: HIGH THROUGHPUT CYTOCHROME P450 GENOTYPING
; FILE REFERENCE: 034827-1303
; CURRENT APPLICATION NUMBER: US/10/615,497
; CURRENT FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-10-615-497-9

Query Match 100.0%; Score 17; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
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Db 1 CGCATCTCCCACCCCCA 17

RESULT 2
US-10-411-954-36
; Sequence 36, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-36

Query Match 100.0%; Score 17; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
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Db 7 CGCATCTCCCACCCCCA 23

RESULT 3
US-10-617-070-36
; Sequence 36, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-36

Query Match 100.0%; Score 17; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 7 CGCATCTCCCACCCCCA 23

RESULT 4
US-10-956-507-36
; Sequence 36, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/617,070
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-36

Query Match 100.0%; Score 17; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 7 CGCATCTCCCACCCCCA 23

RESULT 5
US-10-411-954-66
; Sequence 66, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-66

Query Match 100.0%; Score 17; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24
```

RESULT 6
US-10-411-954-288
; Sequence 288, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-288

Query Match 100.0%; Score 17; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24
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RESULT 7
US-10-617-070-66
; Sequence 66, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-66

Query Match 100.0%; Score 17; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24
```

RESULT 8
US-10-617-070-288
; Sequence 288, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-288

Query Match 100.0%; Score 17; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          8 CGCATCTCCCACCCCCA 24
```

RESULT 9
US-10-617-070-368
; Sequence 368, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic
US-10-617-070-368

Query Match 100.0%; Score 17; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 8 CGCATCTCCCACCCCCA 24

RESULT 10
US-10-956-507-66
; Sequence 66, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/617,070
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-66

Query Match 100.0%; Score 17; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 8 CGCATCTCCCACCCCCA 24

RESULT 11
US-10-956-507-288
; Sequence 288, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/617,070
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-288

Query Match 100.0%; Score 17; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 8 CGCATCTCCCACCCCCA 24

RESULT 12
US-10-956-507-368
; Sequence 368, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/617,070
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-368

Query Match 100.0%; Score 17; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 8 CGCATCTCCCACCCCCA 24

RESULT 13
US-10-411-954-252
; Sequence 252, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11

; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 252
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-252

Query Match 100.0%; Score 17; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 1 CGCATCTCCCACCCCCA 17

RESULT 14
US-10-411-954-253
; Sequence 253, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 253
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-253

Query Match 100.0%; Score 17; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 1 CGCATCTCCCACCCCCA 17

RESULT 15
US-10-617-070-252
; Sequence 252, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 252
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-252

Query Match 100.0%; Score 17; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 1 CGCATCTCCCACCCCCA 17

RESULT 16
US-10-617-070-253
; Sequence 253, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 253
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-253

Query Match 100.0%; Score 17; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 1 CGCATCTCCCACCCCCA 17

RESULT 17
US-10-956-507-252
; Sequence 252, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507

```
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: US/10/617,070
;  PRIOR FILING DATE: 2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 252
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-956-507-252

  Query Match             100.0%;  Score 17;  DB 10;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          1 CGCATCTCCCACCCCCA 17


RESULT 18
US-10-956-507-253
; Sequence 253, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/956,507
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: US/10/617,070
;  PRIOR FILING DATE: 2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 253
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-956-507-253

  Query Match             100.0%;  Score 17;  DB 10;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db          1 CGCATCTCCCACCCCCA 17


RESULT 19
US-10-411-954-39/c
; Sequence 39, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  TITLE OF INVENTION: Characterization of CYP2D6 Alleles
;  FILE REFERENCE: FORS-07897
;  CURRENT APPLICATION NUMBER: US/10/411,954
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 356
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-411-954-39

  Query Match             100.0%;  Score 17;  DB 7;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 20
US-10-411-954-40/c
; Sequence 40, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  TITLE OF INVENTION: Characterization of CYP2D6 Alleles
;  FILE REFERENCE: FORS-07897
;  CURRENT APPLICATION NUMBER: US/10/411,954
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 356
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-411-954-40

  Query Match             100.0%;  Score 17;  DB 7;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 21
US-10-617-070-39/c
; Sequence 39, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/617,070
```

; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-39

Query Match 100.0%; Score 17; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 22
US-10-617-070-40/c
; Sequence 40, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-40

Query Match 100.0%; Score 17; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 23
US-10-956-507-39/c
; Sequence 39, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/617,070
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-39

Query Match 100.0%; Score 17; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 24
US-10-956-507-40/c
; Sequence 40, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/617,070
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-40

Query Match 100.0%; Score 17; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 25

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US-10-411-954-69/c
; Sequence 69, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  TITLE OF INVENTION: Characterization of CYP2D6 Alleles
;  FILE REFERENCE: FORS-07897
;  CURRENT APPLICATION NUMBER: US/10/411,954
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 356
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-411-954-69

  Query Match            100.0%;  Score 17;  DB 7;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 26
US-10-411-954-70/c
; Sequence 70, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  TITLE OF INVENTION: Characterization of CYP2D6 Alleles
;  FILE REFERENCE: FORS-07897
;  CURRENT APPLICATION NUMBER: US/10/411,954
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 356
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-411-954-70

  Query Match            100.0%;  Score 17;  DB 7;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 27
US-10-411-954-291/c
; Sequence 291, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  TITLE OF INVENTION: Characterization of CYP2D6 Alleles
;  FILE REFERENCE: FORS-07897
;  CURRENT APPLICATION NUMBER: US/10/411,954
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 356
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 291
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-411-954-291

  Query Match            100.0%;  Score 17;  DB 7;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 28
US-10-411-954-292/c
; Sequence 292, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  TITLE OF INVENTION: Characterization of CYP2D6 Alleles
;  FILE REFERENCE: FORS-07897
;  CURRENT APPLICATION NUMBER: US/10/411,954
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 356
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-411-954-292

  Query Match            100.0%;  Score 17;  DB 7;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 29
US-10-617-070-69/c
; Sequence 69, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/617,070
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
```

; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-69

Query Match 100.0%; Score 17; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 30
US-10-617-070-70/c
; Sequence 70, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-70

Query Match 100.0%; Score 17; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 31
US-10-617-070-291/c
; Sequence 291, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 291
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-291

Query Match 100.0%; Score 17; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 32
US-10-617-070-292/c
; Sequence 292, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-292

Query Match 100.0%; Score 17; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 33
US-10-617-070-371/c
; Sequence 371, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.

; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 371
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-371

Query Match 100.0%; Score 17; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 34
US-10-617-070-372/c
; Sequence 372, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/617,070
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 372
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-617-070-372

Query Match 100.0%; Score 17; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 35
US-10-956-507-69/c
; Sequence 69, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/617,070
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-69

Query Match 100.0%; Score 17; DB 10; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 36
US-10-956-507-70/c
; Sequence 70, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; APPLICANT: Cao, Feng
; APPLICANT: Oldenburg, Mary C.
; APPLICANT: Koelbl, Jim C.
; APPLICANT: Aizenstein, Brian D.
; APPLICANT: Davey, Keith
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
; FILE REFERENCE: FORS-08195
; CURRENT APPLICATION NUMBER: US/10/956,507
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/10/617,070
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-70

Query Match 100.0%; Score 17; DB 10; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 37
US-10-956-507-291/c
; Sequence 291, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/956,507
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: US/10/617,070
;  PRIOR FILING DATE: 2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 291
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-956-507-291

  Query Match           100.0%;  Score 17;  DB 10;  Length 44;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 38
US-10-956-507-292/c
; Sequence 292, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/956,507
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: US/10/617,070
;  PRIOR FILING DATE: 2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-956-507-292

  Query Match           100.0%;  Score 17;  DB 10;  Length 44;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 39
US-10-956-507-371/c
; Sequence 371, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/956,507
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: US/10/617,070
;  PRIOR FILING DATE: 2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 371
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-956-507-371

  Query Match           100.0%;  Score 17;  DB 10;  Length 44;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db         35 CGCATCTCCCACCCCCA 19


RESULT 40
US-10-956-507-372/c
; Sequence 372, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/956,507
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: US/10/617,070
;  PRIOR FILING DATE: 2003-07-10
```

; PRIOR APPLICATION NUMBER: 10/411,954
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 372
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-372

Query Match 100.0%; Score 17; DB 10; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 35 CGCATCTCCCACCCCCA 19

RESULT 41
US-09-880-732-20
; Sequence 20, Application US/09880732
; Patent No. US20020127561A1
; GENERAL INFORMATION:
; APPLICANT: GENICON SCIENCES CORPORATION
; APPLICANT: BEE, Gary
; APPLICANT: KOHNE, David E.
; APPLICANT: KORB, Linda
; APPLICANT: PETERSON, Todd
; APPLICANT: YGUERABIDE, Juan
; TITLE OF INVENTION: ASSAY FOR GENETIC POLYMORPHISMS USING SCATTERED LIGHT DETECTABLE
; FILE REFERENCE: 089498/0403
; CURRENT APPLICATION NUMBER: US/09/880,732
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/210,988
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Exemplary probe for CYP2D6 allele detection
US-09-880-732-20

Query Match 100.0%; Score 17; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 9 CGCATCTCCCACCCCCA 25

RESULT 42
US-09-880-732-21
; Sequence 21, Application US/09880732
; Patent No. US20020127561A1
; GENERAL INFORMATION:
; APPLICANT: GENICON SCIENCES CORPORATION
; APPLICANT: BEE, Gary
; APPLICANT: KOHNE, David E.
; APPLICANT: KORB, Linda
; APPLICANT: PETERSON, Todd
; APPLICANT: YGUERABIDE, Juan
; TITLE OF INVENTION: ASSAY FOR GENETIC POLYMORPHISMS USING SCATTERED LIGHT DETECTABLE
; FILE REFERENCE: 089498/0403
; CURRENT APPLICATION NUMBER: US/09/880,732
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/210,988
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Exemplary probe for CYP2D6 allele detection
US-09-880-732-21

Query Match 100.0%; Score 17; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 9 CGCATCTCCCACCCCCA 25

RESULT 43
US-10-260-638-101
; Sequence 101, Application US/10260638
; Publication No. US20030207327A1
; GENERAL INFORMATION:
; APPLICANT: KMIEC, ERIC B.
; APPLICANT: RICE, MICHAEL C.
; TITLE OF INVENTION: COISOGENIC EUKARYOTIC CELL COLLECTIONS
; FILE REFERENCE: NaPro-12 US
; CURRENT APPLICATION NUMBER: US/10/260,638
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/325,992
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: targeting oligonucleotide
US-10-260-638-101

Query Match 100.0%; Score 17; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 32 CGCATCTCCCACCCCCA 48

RESULT 44
US-10-260-638-102/c
; Sequence 102, Application US/10260638
; Publication No. US20030207327A1
; GENERAL INFORMATION:
; APPLICANT: KMIEC, ERIC B.
; APPLICANT: RICE, MICHAEL C.
; TITLE OF INVENTION: COISOGENIC EUKARYOTIC CELL COLLECTIONS
; FILE REFERENCE: NaPro-12 US
; CURRENT APPLICATION NUMBER: US/10/260,638
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/325,992
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102

; LENGTH: 121
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: targeting oligonucleotide
US-10-260-638-102

Query Match 100.0%; Score 17; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 90 CGCATCTCCCACCCCCA 74

RESULT 45
US-10-156-995-79
; Sequence 79, Application US/10156995
; Publication No. US20030211486A1
; GENERAL INFORMATION:
; APPLICANT: DNA Print Genomics, Inc.
; APPLICANT: FRUDAKIS, Tony N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING POLYMORPHISMS ASSOCIATED W
; TITLE OF INVENTION: PIGMENTATION
; FILE REFERENCE: DNA1140-7
; CURRENT APPLICATION NUMBER: US/10/156,995
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US 60/346,303
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/334,674
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/344,418
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/323,662
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/310,781
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/300,187
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/293,560
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Homo sapiens 869777
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (270)..(270)
; OTHER INFORMATION: n = g or c
US-10-156-995-79

Query Match 100.0%; Score 17; DB 7; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 438 CGCATCTCCCACCCCCA 454

RESULT 46
US-10-188-359-201
; Sequence 201, Application US/10188359
; Publication No. US20030215819A1
; GENERAL INFORMATION:
; APPLICANT: DNA Print Genomics, Inc.
; APPLICANT: FRUDAKIS, Tony N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INFERRING A RESPONSE TO A STATIN
; FILE REFERENCE: DNA1150-3
; CURRENT APPLICATION NUMBER: US/10/188,359
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/301,867
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/310,783
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/322,478
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 201
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Homo sapiens CYP2D6 869777
US-10-188-359-201

Query Match 100.0%; Score 17; DB 7; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 438 CGCATCTCCCACCCCCA 454

RESULT 47
US-10-027-632-150088
; Sequence 150088, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150088
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-150088

Query Match 100.0%; Score 17; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||||||||||||||
Db 337 CGCATCTCCCACCCCCA 353

RESULT 48
US-10-027-632-150089
; Sequence 150089, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

```
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150089
;   LENGTH: 663
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-150089

  Query Match             100.0%;  Score 17;  DB 6;  Length 663;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        337 CGCATCTCCCACCCCCA 353


RESULT 49
US-10-027-632-150088
; Sequence 150088, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150088
;   LENGTH: 663
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-150088

  Query Match             100.0%;  Score 17;  DB 7;  Length 663;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        337 CGCATCTCCCACCCCCA 353


RESULT 50
US-10-027-632-150089
; Sequence 150089, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150089
;   LENGTH: 663
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-150089

  Query Match             100.0%;  Score 17;  DB 7;  Length 663;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        337 CGCATCTCCCACCCCCA 353


RESULT 51
US-10-165-410A-18
; Sequence 18, Application US/10165410A
; Publication No. US20030175728A1
; GENERAL INFORMATION:
;  APPLICANT: Belousov, Yevgeniy S.
;  APPLICANT:  Afonina, Irina A.
;  APPLICANT:  Epoch Biosciences, Inc.
;  TITLE OF INVENTION: Real-Time Linear Detection Probes:  Sensitive 5'-Minor
;  TITLE OF INVENTION:  Groove Binder-Containing Probes for PCR Analysis
;  FILE REFERENCE: 17682A-007220US
;  CURRENT APPLICATION NUMBER: US/10/165,410A
;  CURRENT FILING DATE:  2003-03-17
;  PRIOR APPLICATION NUMBER: US 09/457,616
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: US 09/876,830
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/302,137
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/351,637
;  PRIOR FILING DATE: 2002-01-23
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 900
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: portion of cytochrome P450 2D6 gene (CYP2D6*4
;   OTHER INFORMATION: allele)
US-10-165-410A-18

  Query Match             100.0%;  Score 17;  DB 7;  Length 900;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        448 CGCATCTCCCACCCCCA 464


RESULT 52
US-10-301-480-600536/c
; Sequence 600536, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 600536
;   LENGTH: 995
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-600536

  Query Match             100.0%;  Score 17;  DB 12;  Length 995;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        954 CGCATCTCCCACCCCCA 938


RESULT 53
US-10-301-480-1213945/c
; Sequence 1213945, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1213945
;   LENGTH: 995
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-1213945

  Query Match             100.0%;  Score 17;  DB 12;  Length 995;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        954 CGCATCTCCCACCCCCA 938


RESULT 54
US-10-156-995-75
; Sequence 75, Application US/10156995
; Publication No. US20030211486A1
; GENERAL INFORMATION:
;  APPLICANT: DNA Print Genomics, Inc.
;  APPLICANT:  FRUDAKIS, Tony N.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING POLYMORPHISMS ASSOCIATED W
;  TITLE OF INVENTION:  PIGMENTATION
;  FILE REFERENCE: DNA1140-7
;  CURRENT APPLICATION NUMBER: US/10/156,995
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: US 60/346,303
;  PRIOR FILING DATE: 2002-01-02
;  PRIOR APPLICATION NUMBER: US 60/334,674
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/344,418
;  PRIOR FILING DATE: 2001-10-26
;  PRIOR APPLICATION NUMBER: US 60/323,662
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US 60/310,781
;  PRIOR FILING DATE: 2001-08-07
;  PRIOR APPLICATION NUMBER: US 60/300,187
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/293,560
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
;   LENGTH: 1190
;   TYPE: DNA
;   ORGANISM: Homo sapiens 756251
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (455)..(455)
;   OTHER INFORMATION: n = g or a
US-10-156-995-75

  Query Match             100.0%;  Score 17;  DB 7;  Length 1190;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        438 CGCATCTCCCACCCCCA 454


RESULT 55
US-10-188-359-228
; Sequence 228, Application US/10188359
; Publication No. US20030215819A1
; GENERAL INFORMATION:
;  APPLICANT: DNA Print Genomics, Inc.
;  APPLICANT:  FRUDAKIS, Tony N.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INFERRING A RESPONSE TO A STATIN
;  FILE REFERENCE: DNA1150-3
;  CURRENT APPLICATION NUMBER: US/10/188,359
;  CURRENT FILING DATE:  2002-07-01
;  PRIOR APPLICATION NUMBER: US 60/301,867
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/310,783
;  PRIOR FILING DATE: 2001-08-07
;  PRIOR APPLICATION NUMBER: US 60/322,478
;  PRIOR FILING DATE: 2001-09-13
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
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```
;   LENGTH: 1190
;   TYPE: DNA
;   ORGANISM: Homo sapiens CYP2D6   756251
US-10-188-359-228

  Query Match             100.0%;  Score 17;  DB 7;  Length 1190;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        438 CGCATCTCCCACCCCCA 454


RESULT 56
US-09-747-538-1
; Sequence 1, Application US/09747538
; Patent No. US20020102549A1
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  Katz, David A.
;  APPLICANT:  Gentile-Davey, Maria C.
;  APPLICANT:  Cornwell, Michael C.
;  APPLICANT:  Huff, Jeffrey B.
;  APPLICANT:  Yu, Hong
;  TITLE OF INVENTION: AMPLIFICATION BASED POLYMORPHISM
;  TITLE OF INVENTION:  DETECTION
;  FILE REFERENCE: 6652.US.O1
;  CURRENT APPLICATION NUMBER: US/09/747,538
;  CURRENT FILING DATE:  2000-12-21
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1450
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-747-538-1

  Query Match             100.0%;  Score 17;  DB 3;  Length 1450;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db        298 CGCATCTCCCACCCCCA 314


RESULT 57
US-10-156-995-63
; Sequence 63, Application US/10156995
; Publication No. US20030211486A1
; GENERAL INFORMATION:
;  APPLICANT: DNA Print Genomics, Inc.
;  APPLICANT:  FRUDAKIS, Tony N.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING POLYMORPHISMS ASSOCIATED W
;  TITLE OF INVENTION:  PIGMENTATION
;  FILE REFERENCE: DNA1140-7
;  CURRENT APPLICATION NUMBER: US/10/156,995
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: US 60/346,303
;  PRIOR FILING DATE: 2002-01-02
;  PRIOR APPLICATION NUMBER: US 60/334,674
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/344,418
;  PRIOR FILING DATE: 2001-10-26
;  PRIOR APPLICATION NUMBER: US 60/323,662
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US 60/310,781
;  PRIOR FILING DATE: 2001-08-07
;  PRIOR APPLICATION NUMBER: US 60/300,187
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/293,560
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 2170
;   TYPE: DNA
;   ORGANISM: Homo sapiens 664784
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1177)..(1177)
;   OTHER INFORMATION: n = g or a
US-10-156-995-63

  Query Match             100.0%;  Score 17;  DB 7;  Length 2170;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       1978 CGCATCTCCCACCCCCA 1994


RESULT 58
US-10-156-995-64
; Sequence 64, Application US/10156995
; Publication No. US20030211486A1
; GENERAL INFORMATION:
;  APPLICANT: DNA Print Genomics, Inc.
;  APPLICANT:  FRUDAKIS, Tony N.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING POLYMORPHISMS ASSOCIATED W
;  TITLE OF INVENTION:  PIGMENTATION
;  FILE REFERENCE: DNA1140-7
;  CURRENT APPLICATION NUMBER: US/10/156,995
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: US 60/346,303
;  PRIOR FILING DATE: 2002-01-02
;  PRIOR APPLICATION NUMBER: US 60/334,674
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/344,418
;  PRIOR FILING DATE: 2001-10-26
;  PRIOR APPLICATION NUMBER: US 60/323,662
;  PRIOR FILING DATE: 2001-09-17
;  PRIOR APPLICATION NUMBER: US 60/310,781
;  PRIOR FILING DATE: 2001-08-07
;  PRIOR APPLICATION NUMBER: US 60/300,187
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/293,560
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
;   LENGTH: 2170
;   TYPE: DNA
;   ORGANISM: Homo sapiens 664785
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1185)..(1185)
;   OTHER INFORMATION: n = t or c
US-10-156-995-64

  Query Match             100.0%;  Score 17;  DB 7;  Length 2170;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       1978 CGCATCTCCCACCCCCA 1994


RESULT 59
US-10-712-363-7
; Sequence 7, Application US/10712363
; Publication No. US20040072235A1
; GENERAL INFORMATION:
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;  APPLICANT: Dawson, Elliot P.
;  TITLE OF INVENTION: CYTOCHROME P450 GENETIC VARIATIONS
;  FILE REFERENCE: 13744-2
;  CURRENT APPLICATION NUMBER: US/10/712,363
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: US 60/306,675
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 10/360,790
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: PCT/US03/21468
;  PRIOR FILING DATE: 2003-07-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 4375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-712-363-7

  Query Match             100.0%;  Score 17;  DB 8;  Length 4375;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       1905 CGCATCTCCCACCCCCA 1921


RESULT 60
US-09-942-310-1
; Sequence 1, Application US/09942310
; Publication No. US20030044797A1
; GENERAL INFORMATION:
;  APPLICANT: Risinger, Carl
;  APPLICANT:  Andersson, Maria K.
;  APPLICANT:  Lewander, Tommy
;  APPLICANT:  Olaisson, Erik
;  TITLE OF INVENTION: Detection of CYP2D6 Polymorphisms
;  FILE REFERENCE: GG119.1US
;  CURRENT APPLICATION NUMBER: US/09/942,310
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: GB 0021286.0
;  PRIOR FILING DATE: 2000-08-30
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9432
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-942-310-1

  Query Match             100.0%;  Score 17;  DB 3;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 61
US-10-209-737-1
; Sequence 1, Application US/10209737
; Publication No. US20030083485A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Milos, Patrice M.
;  APPLICANT:  Webb, Suzin M.
;  TITLE OF INVENTION: No. US20030083485A1el Varients Of The Human CYP2D6 Gene
;  FILE REFERENCE: PC11033AGPR
;  CURRENT APPLICATION NUMBER: US/10/209,737
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: US 60/309,111
;  PRIOR FILING DATE: 2001-07-31
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9432
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-209-737-1

  Query Match             100.0%;  Score 17;  DB 6;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 62
US-10-712-363-1
; Sequence 1, Application US/10712363
; Publication No. US20040072235A1
; GENERAL INFORMATION:
;  APPLICANT: Dawson, Elliot P.
;  TITLE OF INVENTION: CYTOCHROME P450 GENETIC VARIATIONS
;  FILE REFERENCE: 13744-2
;  CURRENT APPLICATION NUMBER: US/10/712,363
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: US 60/306,675
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 10/360,790
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: PCT/US03/21468
;  PRIOR FILING DATE: 2003-07-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 9432
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-712-363-1

  Query Match             100.0%;  Score 17;  DB 8;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 63
US-10-209-737-2
; Sequence 2, Application US/10209737
; Publication No. US20030083485A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Milos, Patrice M.
;  APPLICANT:  Webb, Suzin M.
;  TITLE OF INVENTION: No. US20030083485A1el Varients Of The Human CYP2D6 Gene
;  FILE REFERENCE: PC11033AGPR
;  CURRENT APPLICATION NUMBER: US/10/209,737
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: US 60/309,111
;  PRIOR FILING DATE: 2001-07-31
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 9433
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-209-737-2
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  Query Match             100.0%;  Score 17;  DB 6;  Length 9433;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3448 CGCATCTCCCACCCCCA 3464


RESULT 64
US-10-635-780-4
; Sequence 4, Application US/10635780
; Publication No. US20050032070A1
; GENERAL INFORMATION:
;  APPLICANT: EPIDAUROS Biotechnologie AG
;  TITLE OF INVENTION: Polymorphisms in the human gene for CYP2D6 and their use in
;  TITLE OF INVENTION:  diagnostic and therapeutic applications
;  FILE REFERENCE: VOS-43
;  CURRENT APPLICATION NUMBER: US/10/635,780
;  CURRENT FILING DATE:  2003-08-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 9609
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-635-780-4

  Query Match             100.0%;  Score 17;  DB 9;  Length 9609;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3625 CGCATCTCCCACCCCCA 3641


RESULT 65
US-10-712-363-5
; Sequence 5, Application US/10712363
; Publication No. US20040072235A1
; GENERAL INFORMATION:
;  APPLICANT: Dawson, Elliot P.
;  TITLE OF INVENTION: CYTOCHROME P450 GENETIC VARIATIONS
;  FILE REFERENCE: 13744-2
;  CURRENT APPLICATION NUMBER: US/10/712,363
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: US 60/306,675
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 10/360,790
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: PCT/US03/21468
;  PRIOR FILING DATE: 2003-07-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 13278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-712-363-5

  Query Match             100.0%;  Score 17;  DB 8;  Length 13278;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3046 CGCATCTCCCACCCCCA 3062


RESULT 66
US-10-712-363-6
; Sequence 6, Application US/10712363
; Publication No. US20040072235A1
; GENERAL INFORMATION:
;  APPLICANT: Dawson, Elliot P.
;  TITLE OF INVENTION: CYTOCHROME P450 GENETIC VARIATIONS
;  FILE REFERENCE: 13744-2
;  CURRENT APPLICATION NUMBER: US/10/712,363
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: US 60/306,675
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 10/360,790
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: PCT/US03/21468
;  PRIOR FILING DATE: 2003-07-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 13677
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-712-363-6

  Query Match             100.0%;  Score 17;  DB 8;  Length 13677;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db       3426 CGCATCTCCCACCCCCA 3442


RESULT 67
US-10-712-363-4
; Sequence 4, Application US/10712363
; Publication No. US20040072235A1
; GENERAL INFORMATION:
;  APPLICANT: Dawson, Elliot P.
;  TITLE OF INVENTION: CYTOCHROME P450 GENETIC VARIATIONS
;  FILE REFERENCE: 13744-2
;  CURRENT APPLICATION NUMBER: US/10/712,363
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: US 60/306,675
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 10/360,790
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: PCT/US03/21468
;  PRIOR FILING DATE: 2003-07-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 17060
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-712-363-4

  Query Match             100.0%;  Score 17;  DB 8;  Length 17060;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db      13129 CGCATCTCCCACCCCCA 13145


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Job time : 698 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 23:13:26 ; Search time 30.175 Seconds
(without alignments)
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Title: US-10-615-497-9
Perfect score: 17
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	100.0	6001	6	US-10-517-441-129	Sequence 129, App
c	2	17	100.0	6001	6	US-10-517-441-503	Sequence 503, App
	3	16	94.1	1000	7	US-11-266-748A-201742	Sequence 201742,
c	4	15.4	90.6	1169	7	US-11-266-748A-58639	Sequence 58639, A
	5	15.4	90.6	3008	6	US-10-449-902-12786	Sequence 12786, A
c	6	15.4	90.6	5109	7	US-11-266-748A-32557	Sequence 32557, A
c	7	15.4	90.6	5371	7	US-11-266-748A-56152	Sequence 56152, A
c	8	15.4	90.6	6001	6	US-10-517-441-777	Sequence 777, App
	9	15.4	90.6	201239	7	US-11-266-748A-22854	Sequence 22854, A
	10	15.4	90.6	1237661	7	US-11-266-748A-29041	Sequence 29041, A
	11	15	88.2	314	7	US-11-266-748A-4939	Sequence 4939, Ap
	12	15	88.2	321	7	US-11-266-748A-362089	Sequence 362089,
c	13	15	88.2	321	7	US-11-266-748A-445468	Sequence 445468,
c	14	15	88.2	468	7	US-11-266-748A-70900	Sequence 70900, A
	15	15	88.2	468	7	US-11-266-748A-123711	Sequence 123711,
c	16	15	88.2	607	6	US-10-488-619-463	Sequence 463, App
	17	15	88.2	775	7	US-11-266-748A-253150	Sequence 253150,
c	18	15	88.2	775	7	US-11-266-748A-313667	Sequence 313667,
	19	15	88.2	1000	7	US-11-266-748A-118107	Sequence 118107,
c	20	15	88.2	1000	7	US-11-266-748A-160271	Sequence 160271,
c	21	15	88.2	1000	7	US-11-266-748A-199430	Sequence 199430,
	22	15	88.2	1000	7	US-11-266-748A-291078	Sequence 291078,
c	23	15	88.2	1000	7	US-11-266-748A-342507	Sequence 342507,
	24	15	88.2	1000	7	US-11-266-748A-402457	Sequence 402457,
c	25	15	88.2	1000	7	US-11-266-748A-473503	Sequence 473503,
	26	15	88.2	3058	6	US-10-449-902-27798	Sequence 27798, A
	27	15	88.2	3452	6	US-10-449-902-27539	Sequence 27539, A
c	28	15	88.2	267156	7	US-11-266-748A-32012	Sequence 32012, A
c	29	15	88.2	684973	7	US-11-266-748A-32013	Sequence 32013, A
	30	14.4	84.7	381	7	US-11-266-748A-85999	Sequence 85999, A
	31	14.4	84.7	381	7	US-11-266-748A-112116	Sequence 112116,
c	32	14.4	84.7	381	7	US-11-266-748A-138810	Sequence 138810,
	33	14.4	84.7	424	7	US-11-266-748A-295011	Sequence 295011,
c	34	14.4	84.7	424	7	US-11-266-748A-346440	Sequence 346440,
	35	14.4	84.7	424	7	US-11-266-748A-407618	Sequence 407618,
c	36	14.4	84.7	424	7	US-11-266-748A-478664	Sequence 478664,
c	37	14.4	84.7	520	7	US-11-266-748A-8868	Sequence 8868, Ap
	38	14.4	84.7	651	7	US-11-266-748A-59592	Sequence 59592, A
	39	14.4	84.7	672	7	US-11-266-748A-95477	Sequence 95477, A
c	40	14.4	84.7	672	7	US-11-266-748A-148288	Sequence 148288,
c	41	14.4	84.7	776	7	US-11-266-748A-44807	Sequence 44807, A
c	42	14.4	84.7	776	7	US-11-266-748A-209166	Sequence 209166,
	43	14.4	84.7	907	7	US-11-266-748A-366952	Sequence 366952,
c	44	14.4	84.7	907	7	US-11-266-748A-450331	Sequence 450331,
	45	14.4	84.7	918	7	US-11-266-748A-232060	Sequence 232060,

ALIGNMENTS

RESULT 1
US-10-517-441-129/c
; Sequence 129, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 129
; LENGTH: 6001
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-517-441-129

Query Match 100.0%; Score 17; DB 6; Length 6001;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CGCATCTCCCACCCCCA 17
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Db       3105 CGCATCTCCCACCCCCA 3089
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RESULT 2

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US-10-517-441-503/c
; Sequence 503, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
;  APPLICANT: FOEKENS, John
;  APPLICANT:  HARBECK, Nadia
;  APPLICANT:  KOENIG, Thomas
;  APPLICANT:  MAIER, Sabine
;  APPLICANT:  MARTENS, John
;  APPLICANT:  MODEL, Fabian
;  APPLICANT:  NIMMRICH, Inko
;  APPLICANT:  RUJAN, Tamas
;  APPLICANT:  SCHMITT, Armin
;  APPLICANT:  SCHMITT, Manfred
;  APPLICANT:  LOOK, Maxime P.
;  APPLICANT:  MARX, Almuth
;  APPLICANT:  HOEFLER, Heinz
;  TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
;  TITLE OF INVENTION:  proliferative disorders
;  FILE REFERENCE: 47675-93
;  CURRENT APPLICATION NUMBER: US/10/517,441
;  CURRENT FILING DATE:  2004-12-11
;  PRIOR APPLICATION NUMBER: PCT/EP2003/010881
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: DE 10317955.0
;  PRIOR FILING DATE: 2003-04-17
;  PRIOR APPLICATION NUMBER: DE 10300096.8
;  PRIOR FILING DATE: 2003-01-07
;  PRIOR APPLICATION NUMBER: DE 10245779.4
;  PRIOR FILING DATE: 2002-10-01
;  NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 503
;   LENGTH: 6001
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-503

  Query Match             100.0%;  Score 17;  DB 6;  Length 6001;
  Best Local Similarity   100.0%;  Pred. No. 70;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||||||||||||||||
Db       3105 CGCATCTCCCACCCCCA 3089


RESULT 3
US-11-266-748A-201742
; Sequence 201742, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 201742
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-201742

  Query Match             94.1%;  Score 16;  DB 7;  Length 1000;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCCA 17
              ||||||||||||||||
Db        342 GCATCTCCCACCCCCA 357


RESULT 4
US-11-266-748A-58639/c
; Sequence 58639, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58639
;   LENGTH: 1169
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (332)..(332)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (423)..(423)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (791)..(791)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (993)..(993)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1010)..(1011)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1034)..(1034)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1044)..(1044)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1046)..(1046)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1050)..(1050)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1056)..(1056)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1059)..(1059)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1072)..(1072)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1087)..(1087)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1127)..(1127)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1131)..(1132)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1135)..(1136)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1141)..(1143)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1150)..(1152)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1162)..(1166)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1168)..(1168)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-58639

Query Match 90.6%; Score 15.4; DB 7; Length 1169;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||| |||||||||||
Db 477 CGCATTTCCCACCCCCA 461

RESULT 5
US-10-449-902-12786
; Sequence 12786, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12786
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK110134
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-12786

Query Match 90.6%; Score 15.4; DB 6; Length 3008;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGCATCTCCCACCCCCA 17
||||||| |||||||||
Db 255 CGCATCTTCCACCCCCA 271

RESULT 6
US-11-266-748A-32557/c
; Sequence 32557, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32557
; LENGTH: 5109
; TYPE: DNA
; ORGANISM: Homo Sapiens

US-11-266-748A-32557

Query Match 90.6%; Score 15.4; DB 7; Length 5109;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 CGCATCTCCCACCCCCA 17
              |||| ||||||||||||
Db       2430 CGCACCTCCCACCCCCA 2414
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RESULT 7
US-11-266-748A-56152/c
; Sequence 56152, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56152
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-56152

Query Match 90.6%; Score 15.4; DB 7; Length 5371;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 CGCATCTCCCACCCCCA 17
              |||| ||||||||||||
Db       2678 CGCACCTCCCACCCCCA 2662
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RESULT 8
US-10-517-441-777/c
; Sequence 777, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 777
; LENGTH: 6001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-777

Query Match 90.6%; Score 15.4; DB 6; Length 6001;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 CGCATCTCCCACCCCCA 17
              | ||||||||||||||||
Db       3105 CACATCTCCCACCCCCA 3089
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RESULT 9
US-11-266-748A-22854
; Sequence 22854, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22854
; LENGTH: 201239
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-22854

Query Match 90.6%; Score 15.4; DB 7; Length 201239;
Best Local Similarity 94.1%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 CGCATCTCCCACCCCCA 17
              ||||||||||||| |||
Db     130073 CGCATCTCCCACCTCCA 130089


RESULT 10
US-11-266-748A-29041
; Sequence 29041, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29041
;   LENGTH: 1237661
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-29041

  Query Match             90.6%;  Score 15.4;  DB 7;  Length 1237661;
  Best Local Similarity   94.1%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              |||| ||||||||||||
Db    1136823 CGCAGCTCCCACCCCCA 1136839


RESULT 11
US-11-266-748A-4939
; Sequence 4939, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4939
;   LENGTH: 314
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-4939

  Query Match             88.2%;  Score 15;  DB 7;  Length 314;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCC 16
              |||||||||||||||
Db        158 GCATCTCCCACCCCC 172


RESULT 12
US-11-266-748A-362089
; Sequence 362089, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 362089
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-362089

  Query Match             88.2%;  Score 15;  DB 7;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCC 16
              |||||||||||||||
Db        158 GCATCTCCCACCCCC 172


RESULT 13
US-11-266-748A-445468/c
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; Sequence 445468, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 445468
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-445468

Query Match 88.2%; Score 15; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCATCTCCCACCCCC 16
||||||||||||||||
Db 164 GCATCTCCCACCCCC 150

RESULT 14
US-11-266-748A-70900/c
; Sequence 70900, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70900
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315)..(324)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-70900

Query Match 88.2%; Score 15; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCATCTCCCACCCCC 16
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Db 157 GCATCTCCCACCCCC 143

RESULT 15
US-11-266-748A-123711
; Sequence 123711, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123711
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145)..(154)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-123711

Query Match 88.2%; Score 15; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCATCTCCCACCCCC 16
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Db 312 GCATCTCCCACCCCC 326

Search completed: July 1, 2006, 00:05:59
Job time : 31.175 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:17:54 ; Search time 66.5125 Seconds
(without alignments)
478.239 Million cell updates/sec

Title: US-10-615-497-9
Perfect score: 17
Sequence: 1 cgcatctcccacccca 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
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6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	94.1	601	3	US-09-949-016-141001	Sequence 141001,
	2	16	94.1	23856	3	US-09-949-016-15732	Sequence 15732, A
c	3	15.4	90.6	601	3	US-09-949-016-128389	Sequence 128389,
	4	15.4	90.6	601	3	US-09-949-016-157841	Sequence 157841,
	5	15.4	90.6	1140	2	US-08-289-653-2	Sequence 2, Appli
	6	15.4	90.6	2845	2	US-08-289-653-1	Sequence 1, Appli
	7	15.4	90.6	67745	3	US-09-949-016-17251	Sequence 17251, A
	8	15.4	90.6	83516	3	US-09-949-016-15378	Sequence 15378, A
	9	15.4	90.6	191433	3	US-09-949-016-16144	Sequence 16144, A
	10	15	88.2	16	4	US-10-114-908-135	Sequence 135, App
	11	15	88.2	16	4	US-10-114-908-136	Sequence 136, App
c	12	15	88.2	386	4	US-09-880-107-1169	Sequence 1169, Ap
	13	15	88.2	11495	3	US-09-056-105-9	Sequence 9, Appli
	14	15	88.2	12309	3	US-09-949-016-13709	Sequence 13709, A
	15	15	88.2	16389	3	US-09-741-154-3	Sequence 3, Appli
	16	15	88.2	16389	3	US-10-187-900-3	Sequence 3, Appli
c	17	15	88.2	17154	3	US-09-949-016-16889	Sequence 16889, A
c	18	15	88.2	84571	3	US-09-949-016-17420	Sequence 17420, A
c	19	15	88.2	146307	3	US-09-949-016-14881	Sequence 14881, A
c	20	15	88.2	146307	3	US-09-949-016-14882	Sequence 14882, A
c	21	15	88.2	146307	3	US-09-949-016-14883	Sequence 14883, A
c	22	15	88.2	146307	3	US-09-949-016-14884	Sequence 14884, A
c	23	15	88.2	146307	3	US-09-949-016-14885	Sequence 14885, A
c	24	15	88.2	146307	3	US-09-949-016-14886	Sequence 14886, A
c	25	15	88.2	146307	3	US-09-949-016-14887	Sequence 14887, A
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c	27	15	88.2	148405	3	US-09-949-016-11747	Sequence 11747, A
c	28	15	88.2	148405	3	US-09-949-016-12835	Sequence 12835, A
c	29	15	88.2	148405	3	US-09-949-016-12836	Sequence 12836, A
c	30	15	88.2	148405	3	US-09-949-016-12837	Sequence 12837, A
c	31	15	88.2	178883	3	US-09-949-016-12733	Sequence 12733, A
c	32	15	88.2	178884	3	US-09-949-016-13039	Sequence 13039, A
c	33	14.4	84.7	454	3	US-09-513-999C-3659	Sequence 3659, Ap
	34	14.4	84.7	601	3	US-09-949-016-32887	Sequence 32887, A
c	35	14.4	84.7	601	3	US-09-949-016-58172	Sequence 58172, A
c	36	14.4	84.7	601	3	US-09-949-016-66112	Sequence 66112, A
c	37	14.4	84.7	601	3	US-09-949-016-66113	Sequence 66113, A
c	38	14.4	84.7	601	3	US-09-949-016-91295	Sequence 91295, A
c	39	14.4	84.7	601	3	US-09-949-016-91296	Sequence 91296, A
	40	14.4	84.7	601	3	US-09-949-016-93413	Sequence 93413, A
	41	14.4	84.7	601	3	US-09-949-016-104755	Sequence 104755,
	42	14.4	84.7	601	3	US-09-949-016-104757	Sequence 104757,
	43	14.4	84.7	601	3	US-09-949-016-113757	Sequence 113757,
	44	14.4	84.7	601	3	US-09-949-016-113758	Sequence 113758,
	45	14.4	84.7	601	3	US-09-949-016-113925	Sequence 113925,

ALIGNMENTS

RESULT 1
US-09-949-016-141001
; Sequence 141001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141001
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-141001

Query Match 94.1%; Score 16; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 GCATCTCCCACCCCCA 17
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Db        218 GCATCTCCCACCCCCA 233
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RESULT 2
US-09-949-016-15732
; Sequence 15732, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15732
;   LENGTH: 23856
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(23856)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15732

  Query Match             94.1%;  Score 16;  DB 3;  Length 23856;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCATCTCCCACCCCCA 17
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Db      15271 GCATCTCCCACCCCCA 15286


RESULT 3
US-09-949-016-128389/c
; Sequence 128389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128389
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-128389

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 601;
  Best Local Similarity   94.1%;  Pred. No. 4.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              | ||||||||||||||||
Db        283 CTCATCTCCCACCCCCA 267


RESULT 4
US-09-949-016-157841
; Sequence 157841, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 157841
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-157841

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 601;
  Best Local Similarity   94.1%;  Pred. No. 4.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
              ||||||||||||| |||
Db        427 CGCATCTCCCACCTCCA 443


RESULT 5
US-08-289-653-2
; Sequence 2, Application US/08289653
; Patent No. 5543322
;  GENERAL INFORMATION:
;    APPLICANT:  Kazuaki KITANO et al.
;    TITLE OF INVENTION:  DNA AND ITS USE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/289,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/887,284
;      FILING DATE:  May 22, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1140 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Fusarium sp.
;      STRAIN:  S-19-5 (IFO 8884)
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
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;       CELL TYPE:
;       CELL LINE:
;       ORGANELLE:
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:
;       MAP POSITION:
;       UNITS:
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:
US-08-289-653-2

  Query Match             90.6%;  Score 15.4;  DB 2;  Length 1140;
  Best Local Similarity   94.1%;  Pred. No. 4.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db        337 CGCATCTCCCACCGCCA 353


RESULT 6
US-08-289-653-1
; Sequence 1, Application US/08289653
; Patent No. 5543322
;  GENERAL INFORMATION:
;    APPLICANT:  Kazuaki KITANO et al.
;    TITLE OF INVENTION:  DNA AND ITS USE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/289,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/887,284
;      FILING DATE:  May 22, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2845 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Fusarium sp.
;      STRAIN:  S-19-5 (IFO 8884)
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-289-653-1

  Query Match             90.6%;  Score 15.4;  DB 2;  Length 2845;
  Best Local Similarity   94.1%;  Pred. No. 4.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db        934 CGCATCTCCCACCGCCA 950


RESULT 7
US-09-949-016-17251
; Sequence 17251, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17251
;   LENGTH: 67745
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(67745)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17251

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 67745;
  Best Local Similarity   94.1%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db      42845 CGCCTCTCCCACCCCCA 42861


RESULT 8
US-09-949-016-15378
; Sequence 15378, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15378
;   LENGTH: 83516
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15378

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 83516;
  Best Local Similarity   94.1%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db      68600 CTCATCTCCCACCCCCA 68616


RESULT 9
US-09-949-016-16144
; Sequence 16144, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16144
;   LENGTH: 191433
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16144

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 191433;
  Best Local Similarity   94.1%;  Pred. No. 4.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCATCTCCCACCCCCA 17
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Db     120643 CGCATCTCCCACCTCCA 120659


RESULT 10
US-10-114-908-135
; Sequence 135, Application US/10114908
; Patent No. 6986992
; GENERAL INFORMATION:
;  APPLICANT: Luehrsen, Kenneth R.
;  TITLE OF INVENTION: P450 Single Nucleotide Polymorphism Biochip Analysis
;  FILE REFERENCE: A-70398-1/RMS/DLR
;  CURRENT APPLICATION NUMBER: US/10/114,908
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: US 60/280,583
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 277
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-114-908-135

  Query Match             88.2%;  Score 15;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CATCTCCCACCCCCA 17
              |||||||||||||||
Db          1 CATCTCCCACCCCCA 15


RESULT 11
US-10-114-908-136
; Sequence 136, Application US/10114908
; Patent No. 6986992
; GENERAL INFORMATION:
;  APPLICANT: Luehrsen, Kenneth R.
;  TITLE OF INVENTION: P450 Single Nucleotide Polymorphism Biochip Analysis
;  FILE REFERENCE: A-70398-1/RMS/DLR
;  CURRENT APPLICATION NUMBER: US/10/114,908
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: US 60/280,583
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 277
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 136
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-114-908-136

  Query Match             88.2%;  Score 15;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CATCTCCCACCCCCA 17
              |||||||||||||||
Db          1 CATCTCCCACCCCCA 15
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RESULT 12
US-09-880-107-1169/c
; Sequence 1169, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1169
;   LENGTH: 386
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. 6974667 AA454733
US-09-880-107-1169

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Qy          2 GCATCTCCCACCCCC 16
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Db        158 GCATCTCCCACCCCC 144


RESULT 13
US-09-056-105-9
; Sequence 9, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
;  APPLICANT: KIPPS, THOMAS J.
;  APPLICANT: WU, YUNQI
;  TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
;  TITLE OF INVENTION: PROCESSING
;  FILE REFERENCE: 233/221
;  CURRENT APPLICATION NUMBER: US/09/056,105
;  CURRENT FILING DATE: 1998-04-06
;  EARLIER APPLICATION NUMBER: 60/043,467
;  EARLIER FILING DATE: 1997-04-10
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 11495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-056-105-9

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CATCTCCCACCCCCA 17
              |||||||||||||||
Db       1331 CATCTCCCACCCCCA 1345


RESULT 14
US-09-949-016-13709
; Sequence 13709, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13709
;   LENGTH: 12309
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13709

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CATCTCCCACCCCCA 17
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Db       8813 CATCTCCCACCCCCA 8827


RESULT 15
US-09-741-154-3
; Sequence 3, Application US/09741154
; Patent No. 6437110
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen M. et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001061
;  CURRENT APPLICATION NUMBER: US/09/741,154
;  CURRENT FILING DATE:  2000-12-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 16389
;   TYPE: DNA
;   ORGANISM: Human
US-09-741-154-3

  Query Match           88.2%;  Score 15;  DB 3;  Length 16389;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CATCTCCCACCCCCA 17
              |||||||||||||||
Db      12894 CATCTCCCACCCCCA 12908


Search completed: July  1, 2006, 01:23:17
Job time : 69.5125 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:12:31 ; Search time 957.45 Seconds
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1736.522 Million cell updates/sec

Title: US-10-615-497-11
Perfect score: 26
Sequence: 1 gactcagcctcgtcacctcaccacag 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	92.3	9432	2	AX959041	AX959041 Sequence
	2	24	92.3	9432	2	AX394456	AX394456 Sequence
	3	24	92.3	9432	2	AX687027	AX687027 Sequence
	4	24	92.3	9432	5	HUMCYP2D6	M33388 Human cytoc
	5	24	92.3	9433	2	AX687028	AX687028 Sequence
	6	24	92.3	20337	5	DQ211354	DQ211354 Homo sapi
	7	24	92.3	23381	5	DQ211353	DQ211353 Homo sapi
c	8	24	92.3	133246	5	BX247885	BX247885 Human DNA
	9	22	84.6	2788	2	AX959039	AX959039 Sequence
	10	20.8	80.0	2104	13	AK112693	AK112693 Ciona int
	11	20.8	80.0	139431	5	CT573219	CT573219 CH250-18D
c	12	20.8	80.0	144218	5	CT573094	CT573094 CH250-64B
c	13	20.8	80.0	192018	12	AC116432	AC116432 Papio anu
c	14	20.8	80.0	193301	12	AC147059	AC147059 Pan trogl
c	15	20.2	77.7	110000	15	CP000249_24	Continuation (25 o
	16	20.2	77.7	136000	5	AC055739	AC055739 Homo sapi
c	17	20.2	77.7	150353	12	AC068978	AC068978 Homo sapi
c	18	19.8	76.2	829	6	RATMHEBC	M12382 Rat MHC RT1
c	19	19.8	76.2	1100	6	AF084932	AF084932 Rattus no
c	20	19.8	76.2	1118	6	AF084933	AF084933 Rattus no
c	21	19.8	76.2	1120	6	AF084934	AF084934 Rattus no
c	22	19.8	76.2	1120	6	BC087691	BC087691 Rattus no
	23	19.8	76.2	99964	12	RN364I06	AL732652 Rattus no
	24	19.8	76.2	111298	12	RN99A23	AL603729 Rattus no
	25	19.8	76.2	165087	12	AC158456	AC158456 Rhinoloph
	26	19.8	76.2	171536	12	AC168201	AC168201 Rhinoloph
c	27	19.8	76.2	178948	11	AL929434	AL929434 Zebrafish
c	28	19.8	76.2	183256	12	CR847507	CR847507 Danio rer
	29	19.8	76.2	224292	12	AC026873	AC026873 Homo sapi
c	30	19.8	76.2	224373	12	AC098129	AC098129 Rattus no
	31	19.8	76.2	251251	12	AC120734	AC120734 Rattus no
c	32	19.8	76.2	347664	6	BX883043	BX883043 Rattus no
	33	19.6	75.4	595	5	HSA133731	AJ133731 Homo sapi
	34	19.6	75.4	38911	5	AC005559	AC005559 Homo sapi
	35	19.6	75.4	155060	12	AC140158	AC140158 Felis cat
	36	19.6	75.4	156383	12	AC135221	AC135221 Felis cat
c	37	19.6	75.4	212724	6	AC125252	AC125252 Mus muscu
	38	19.6	75.4	220309	12	AC156872	AC156872 Bos tauru
c	39	19.6	75.4	236086	12	AC098408	AC098408 Rattus no
	40	19.6	75.4	237411	12	AC127402	AC127402 Rattus no
	41	19.6	75.4	285586	12	AC158818	AC158818 Bos tauru
c	42	19.4	74.6	101220	5	AC092372	AC092372 Homo sapi
	43	19.4	74.6	134365	5	AC012624	AC012624 Homo sapi
c	44	19.4	74.6	143079	12	AC021449	AC021449 Homo sapi
	45	19.4	74.6	145659	12	AC008531	AC008531 Homo sapi

ALIGNMENTS

RESULT 1
AX959041
LOCUS AX959041 9432 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 50 from Patent WO03100091.
ACCESSION AX959041
VERSION AX959041.1 GI:40879771
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Brockmoeller,H.J.
TITLE Means and methods for improved treatment using setrones
JOURNAL Patent: WO 03100091-A 50 04-DEC-2003;
Epidauros Biotechnologie AG (DE)
FEATURES Location/Qualifiers
source 1. .9432
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 92.3%; Score 24; DB 2; Length 9432;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CTCAGCCTCGTCACCTCACCACAG 26
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Db 6433 CTCAGCCTCGTCACCTCACCACAG 6456

RESULT 2
AX394456
LOCUS AX394456 9432 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1 from Patent WO0218638.
ACCESSION AX394456
VERSION AX394456.1 GI:21065594
KEYWORDS .
SOURCE Homo sapiens (human)

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
  TITLE     Detection of cyp2d6 polymorphisms
  JOURNAL   Patent: WO 0218638-A 1 07-MAR-2002;
            Gemini Genomics PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .9432
                     /organism="Homo sapiens"
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ORIGIN

  Query Match             92.3%;  Score 24;  DB 2;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 3
AX687027
LOCUS       AX687027               9432 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1 from Patent EP1281755.
ACCESSION   AX687027
VERSION     AX687027.1  GI:29409531
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Milos,P.M. and Webb,S.M.
  TITLE     Variants of the human cyp2d6 gene
  JOURNAL   Patent: EP 1281755-A 1 05-FEB-2003;
            Pfizer Products Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             92.3%;  Score 24;  DB 2;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 4
HUMCYP2D6
LOCUS       HUMCYP2D6              9432 bp    DNA     linear   PRI 22-NOV-1994
DEFINITION  Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
ACCESSION   M33388
VERSION     M33388.1  GI:181303
KEYWORDS    cytochrome P450; cytochrome P450 IID6.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 9432)
  AUTHORS   Kimura,S., Umeno,M., Skoda,R.C., Meyer,U.A. and Gonzalez,F.J.
  TITLE     The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and
            identification of the polymorphic CYP2D6 gene, a related gene, and
            a pseudogene
  JOURNAL   Am. J. Hum. Genet. 45 (6), 889-904 (1989)
  PUBMED    2574001
COMMENT     Original source text: Human DNA, clone lambda2D-18/2.
            Draft entry and computer-readable sequence for [Am. J. Hum. Genet.
            45, 889-904 (1989)] kindly submitted
            by S.Kimura, 29-MAR-1990.
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="22q13.1"
     gene            join(1532. .1799,2503. .2674,3225. .3377,3466. .3626,
                     4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5909)
                     /gene="CYP2D6"
     mRNA            join(1532. .1799,2503. .2674,3225. .3377,3466. .3626,
                     4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5909)
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                     /product="cytochrome P450 IID6"
                     /note="G00-132-127"
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                     /note="cytochrome P450 IID6; G00-132-127"
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                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
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                     /note="G00-132-127; does not fit consensus"
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                     /note="G00-132-127"
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                     /note="G00-132-127"
                     /number=3
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 5
AX687028
LOCUS       AX687028               9433 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2 from Patent EP1281755.
ACCESSION   AX687028
VERSION     AX687028.1  GI:29409532
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Milos,P.M. and Webb,S.M.
  TITLE     Variants of the human cyp2d6 gene
  JOURNAL   Patent: EP 1281755-A 2 05-FEB-2003;
            Pfizer Products Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9433
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                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             92.3%;  Score 24;  DB 2;  Length 9433;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6434 CTCAGCCTCGTCACCTCACCACAG 6457


RESULT 6
DQ211354
LOCUS       DQ211354               20337 bp    DNA     linear   PRI 21-OCT-2005
DEFINITION  Homo sapiens cytochrome P450 2D7 (CYP2D7P) pseudogene, partial
            sequence; and cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*10 allele,
            complete cds.
ACCESSION   DQ211354
VERSION     DQ211354.1  GI:77732537
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 20337)
  AUTHORS   Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K.,
            Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
  TITLE     Sequence-based analysis of the CYP2D6*36-CYP2D6*10 tandem-type
            arrangement, a major CYP2D6*10-harboring haplotype in the Japanese
            population
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 20337)
  AUTHORS   Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K.,
            Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-2005) Team for Pharmacogenetics, National
            Institute of Health Sciences, 1-18-1, Kamiyoga, Setagaya-ku, Tokyo
            158-8501, Japan
FEATURES             Location/Qualifiers
     source          1. .20337
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <429. .3022
                     /gene="CYP2D7P"
                     /pseudo
     CDS             join(<429. .581,670. .831,1257. .1433,1626. .1767,1962. .2149,
                     2604. .2745,2844. .3022)
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                     /note="cytochrome P450 2D7"
                     /pseudo
                     /codon_start=3
     gene            <12513. .>16730
                     /gene="CYP2D6"
                     /allele="CYP2D6*10"
     mRNA            join(<12513. .12692,13395. .13566,14119. .14271,14360. .14520,
                     14954. .15130,15321. .15462,15670. .15857,16312. .16453,
                     16552. .>16730)
                     /gene="CYP2D6"
                     /allele="CYP2D6*10"
                     /product="cytochrome P450 2D6"
     CDS             join(12513. .12692,13395. .13566,14119. .14271,14360. .14520,
                     14954. .15130,15321. .15462,15670. .15857,16312. .16453,
                     16552. .16730)
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                     /allele="CYP2D6*10"
                     /EC_number="1.14.14.1"
                     /note="debrisoquine 4-hydroxylase"
                     /codon_start=1
                     /product="cytochrome P450 2D6"
                     /protein_id="ABB01372.1"
                     /db_xref="GI:77732538"
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                     NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
                     PVPITQILGFGPRSQGVFLARYGPAWREQRRFSVSTLRNLGLGKKSLEQWVTEEAACL
                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
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ORIGIN

  Query Match             92.3%;  Score 24;  DB 5;  Length 20337;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
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Db      17327 CTCAGCCTCGTCACCTCACCACAG 17350


RESULT 7
DQ211353
LOCUS       DQ211353               23381 bp    DNA     linear   PRI 19-OCT-2005
DEFINITION  Homo sapiens cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*36 allele
            and cytochrome P450 2D6 (CYP2D6) gene, CYP2D6*10 allele, complete
            cds.
ACCESSION   DQ211353
VERSION     DQ211353.1  GI:77732534
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 23381)
  AUTHORS   Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K.,
            Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
  TITLE     Sequence-based analysis of the CYP2D6*36-CYP2D6*10 tandem-type
            arrangement, a major CYP2D6*10-harboring haplotype in the Japanese
            population
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 23381)
  AUTHORS   Soyama,A., Saito,Y., Kubo,T., Miyajima,A., Ohno,Y., Komamura,K.,
            Kamakura,S., Kitakaze,M., Tomoike,H., Ozawa,S. and Sawada,J.-I.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-2005) Team for Pharmacogenetics, National
            Institute of Health Sciences, 1-18-1, Kamiyoga, Setagaya-ku, Tokyo
            158-8501, Japan
FEATURES             Location/Qualifiers
     source          1. .23381
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /map="22q13.31"
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                     /gene="CYP2D6"
                     /allele="CYP2D6*36"
     mRNA            join(<1849. .2028,2731. .2902,3455. .3607,3696. .3856,
                     4290. .4466,4657. .4798,5006. .5193,5648. .5789,5888. .>6066)
                     /gene="CYP2D6"
                     /allele="CYP2D6*36"
                     /product="cytochrome P450 2D6"
     CDS             join(1849. .2028,2731. .2902,3455. .3607,3696. .3856,
                     4290. .4466,4657. .4798,5006. .5193,5648. .5789,5888. .6066)
                     /gene="CYP2D6"
                     /allele="CYP2D6*36"
                     /EC_number="1.14.14.1"
                     /note="debrisoquine 4-hydroxylase"
                     /codon_start=1
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                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
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                TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
                MELFLFFTSLLQHFSFSVAAGQPRPSHSRVVSFLVTPSPYELCAVPR"
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                     /allele="CYP2D6*10"
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                     19596. .>19774)
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                     17998. .18174,18365. .18506,18714. .18901,19356. .19497,
                     19596. .19774)
                     /gene="CYP2D6"
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                     /EC_number="1.14.14.1"
                     /note="debrisoquine 4-hydroxylase"
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                     CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
                     FLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFL
                     AEMEKAKGNPESSFNDENLRIVVADLFSAGMVTTSTTLAWGLLLMILHPDVQRRVQQE
                     IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKG
                     TTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEPLAR
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ORIGIN

  Query Match             92.3%;  Score 24;  DB 5;  Length 23381;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
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Db      20371 CTCAGCCTCGTCACCTCACCACAG 20394


RESULT 8
BX247885/c
LOCUS       BX247885               133246 bp    DNA     linear   PRI 18-MAY-2005
DEFINITION  Human DNA sequence from clone RP4-669P10 on chromosome
            22q13.31-13.33, complete sequence.
ACCESSION   BX247885
VERSION     BX247885.11  GI:30524848
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 133246)
  AUTHORS   Lloyd,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On May 10, 2003 this sequence version replaced gi:30230961.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 22, constructed by the Sanger Centre Chromosome 22
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr22
            RP4-669P10 is from the library RPCI-4 constructed by the group of
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          Pieter de Jong. For further details see
          http://www.chori.org/bacpac/home.htm
          VECTOR: pCYPAC2
          -------------- Genome Center
          Center: Wellcome Trust Sanger Institute
          Center code: SC
          Web site: http://www.sanger.ac.uk
          Contact: vega@sanger.ac.uk
          --------------
          This sequence was finished as follows unless otherwise noted: all
          regions were either double-stranded or sequenced with an alternate
          chemistry or covered by high quality data (i.e., phred quality >=
          30); an attempt was made to resolve all sequencing problems, such
          as compressions and repeats; all regions were covered by at least
          one subclone; and the assembly was confirmed by restriction digest,
          except on the rare occasion of the clone being a YAC.
FEATURES             Location/Qualifiers
     source          1. .133246
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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     misc_feature    1
                     /note="Clone_left_end: RP4-669P10"
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     mRNA            join(3534. .3617,4007. .4049,4362. .4513)
                     /locus_tag="RP4-669P10.8-006"
     gene            join(5457. .6236,7326. .7467,7658. .7834,8268. .8428,
                     20048. .20189,20644. .20831,22211. .22363,22727. .22839,
                     22883. .23087,23767. .23947)
                     /locus_tag="RP4-669P10.1-001"
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                     20048. .20189,20644. .20831,22211. .22363,22727. .22839,
                     22883. .23087,23767. .23947)
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                     /codon_start=1
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                     /note="Single clone region. Sequence generated from a
                     transposon library derived from a single pUC clone.
                     Restriction digest data confirm the assembly."
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     gene            complement(join(29359. .29537,29636. .29777,30228. .30412,
                     30617. .30758,30945. .31121,31569. .31731,31820. .31972,
                     32521. .32692,34313. .34489))
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     CDS             complement(join(29359. .29537,29636. .29777,30228. .30412,
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                     /locus_tag="RP4-669P10.5-001"
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     gene            complement(join(39501. .40846,48097. .48224,49335. .49384,
                     59097. .59190,89139. .94930))
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                     59097. .59190,89139. .94930))
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     gene            complement(join(<39564. .40846,48097. .48224,49335. .49384,
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                     AU017455 H55457 H55458
                     match: cDNAs: U19345 U20282"
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                     PQERKTQDVGMAVSMDTISIVTMWGEGGG"
     CDS             complement(join(48141. .48224,49335. .49384,59097. .59190,
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                     GENLQCGQGSVPMGSRNRILQLMPQLSPTPSMMPSPNSHAAGFKGFGLEGVPEKRLTD
                     PGLSSLSALSTQVANLPNTVQHMLLSDALTPQKKTSKRPSSSKKADSCTNSEGSSQPE
                     EQLKSPMAESLDGGCSSSSEDQGERVRQLSGQSTSSDTTYKGGASEKAGSSPAQGAQN
                     EPPRLNASPAAREEATSPGAKDMPLSSDGNPKVNEKTVGVIVSREAMTGRVEKPGGQD
                     KGSQEDDPAATQRPPSNGGAKETSHASLPQPEPPGGGGSKGNKNGDNNSNHNGEGNGQ
                     SGHSAAGPGFTSRTEPSKSPGSLRYSYKDSFGSAVPRNVSGFPQYPTGQEKGDFTGHG
                     ERKGRNEKFPSLLQEVLQGYHHHPDRRYSRSTQEHQGMAGSLEGTTRPNVLVSQTNEL
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                     HHMNPHMTFSERANRSSLHTPFSPNSETLASAYHANTRAHAYGDPNAGLNSQLHYKRQ
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                     KNVPPVGILAPEANPKAEEKENDTVTISPKQEGFPPKGYFPSGKKKGRPIGSVNKQKK
                     QQQPPPPPPQPPQIPEGSADGEPKPKKQRQRRERRKPGAQPRKRKTKQAVPIVEPQEP
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                     SLTPPPSSTESKALPASSFMLQGPVVTESSVMGHLVCCLCGKWASYRNMGDLFGPFYP
                     QDYAATLPKNPPPKRATEMQSKVKVRHKSASNGSKTDTEEEEEQQQQQKEQRSLAAHP
                     RFKRRHRSEDCGGGPRSLSRGLPCKKAATEGSSEKTVLDSKPSVPTTSEGGPELELQI
                     PELPLDSNEFWVHEGCILWANGIYLVCGRLYGLQEALEIAREMKCSHCQEAGATLGCY
                     NKGCSFRYHYPCAIDADCLLHEENFSVRCPKHKPPLPCPLPPLQNKTAKGSLSTEQSE
                     RG"
     CDS             complement(join(48141. .48224,49335. .49384,59097. .>59190))
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                     /translation="KCSHCQEAGATLGCYNKGCSFRYHYPCAIDADCLLHEENFSVRC
                     PKHKPPLPCPLPPLQNKTAKGSLSTEQSERG"
     misc_feature    133246
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ORIGIN

  Query Match             92.3%;  Score 24;  DB 5;  Length 133246;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       5464 CTCAGCCTCGTCACCTCACCACAG 5441


RESULT 9
AX959039
LOCUS       AX959039               2788 bp    DNA     linear   PAT 14-JAN-2004
DEFINITION  Sequence 48 from Patent WO03100091.
ACCESSION   AX959039
VERSION     AX959039.1  GI:40879769
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Brockmoeller,H.J.
  TITLE     Means and methods for improved treatment using setrones
  JOURNAL   Patent: WO 03100091-A 48 04-DEC-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .2788
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             84.6%;  Score 22;  DB 2;  Length 2788;
  Best Local Similarity   100.0%;  Pred. No. 9.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||
Db          1 CAGCCTCGTCACCTCACCACAG 22


RESULT 10
AK112693
LOCUS       AK112693               2104 bp    mRNA    linear   INV 30-NOV-2002
DEFINITION  Ciona intestinalis cDNA, clone:cieg032p16, full insert sequence.
ACCESSION   AK112693
VERSION     AK112693.1  GI:23576088
KEYWORDS    FLI_CDNA.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1
  AUTHORS   Satou,Y., Yamada,L., Mochizuki,Y., Takatori,N., Kawashima,T.,
            Sasaki,A., Hamaguchi,M., Awazu,S., Yagi,K., Sasakura,Y.,
            Nakayama,A., Ishikawa,H., Inaba,K. and Satoh,N.
  TITLE     A cDNA resource from the basal chordate Ciona intestinalis
  JOURNAL   Genesis 33 (4), 153-154 (2002)
   PUBMED   12203911
REFERENCE   2  (bases 1 to 2104)
  AUTHORS   Satou,Y. and Satoh,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-OCT-2002) Nori Satoh, Kyoto University, Department of
            Zoology; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            (E-mail:satoh@ascidian.zool.kyoto-u.ac.jp, Tel:81-75-753-4095,
            Fax:81-75-705-1113)
COMMENT     Ciona intestinalis cDNA Project (URL:
            http://ghost.zool.kyoto-u.ac.jp/indexr1.html).
FEATURES             Location/Qualifiers
     source          1. .2104
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cieg032p16"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 13;  Length 2104;
  Best Local Similarity   91.7%;  Pred. No. 39;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db       1681 GACACAGCCTCGTCATCTCACCAC 1704


RESULT 11
CT573219
LOCUS       CT573219               139431 bp    DNA     linear   PRI 08-FEB-2006
DEFINITION  CH250-18D2, complete sequence.
ACCESSION   CT573219
VERSION     CT573219.3  GI:87080522
KEYWORDS    HTG.
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 139431)
  AUTHORS   Berg,C., Conrad,A., Loehnert,T.H., Nordsiek,G., Severitt,S.,
            Scharfe,M., Schindewolf,C., Schrader,F., Thies,S. and Bloecker,H.
  TITLE     direct submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 139431)
  AUTHORS   Berg,C., Conrad,A., Loehnert,T.H., Nordsiek,G., Severitt,S.,
            Scharfe,M., Schindewolf,C., Schrader,F., Thies,S. and Bloecker,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JAN-2006) Dept. of Genome Analysis, German Research
            Centre for Biotechnology, Mascheroder Weg 1, Braunschweig D-38124,
            Germany
COMMENT     On Feb 8, 2006 this sequence version replaced gi:86197631.
FEATURES             Location/Qualifiers
     source          1. .139431
                     /organism="Macaca mulatta"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9544"
                     /chromosome="9"
                     /clone="CH250-18D2"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 5;  Length 139431;
  Best Local Similarity   91.7%;  Pred. No. 1.1e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              |||| || ||||||||||||||||
Db     134740 CTCAACCACGTCACCTCACCACAG 134763


RESULT 12
CT573094/c
LOCUS       CT573094               144218 bp    DNA     linear   PRI 08-FEB-2006
DEFINITION  CH250-64B17, complete sequence.
ACCESSION   CT573094
VERSION     CT573094.2  GI:85857276
KEYWORDS    HTG.
```

```
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 144218)
  AUTHORS   Berg,C., Conrad,A., Loehnert,T.H., Nordsiek,G., Severitt,S.,
            Scharfe,M., Schindewolf,C., Schrader,F., Thies,S. and Bloecker,H.
  TITLE     direct submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 144218)
  AUTHORS   Berg,C., Conrad,A., Loehnert,T.H., Nordsiek,G., Severitt,S.,
            Scharfe,M., Schindewolf,C., Schrader,F., Thies,S. and Bloecker,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JAN-2006) Dept. of Genome Analysis, German Research
            Centre for Biotechnology, Mascheroder Weg 1, Braunschweig D-38124,
            Germany
COMMENT     On Jan 27, 2006 this sequence version replaced gi:84871848.
FEATURES             Location/Qualifiers
     source          1. .144218
                     /organism="Macaca mulatta"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9544"
                     /chromosome="9"
                     /clone="CH250-64B17"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 5;  Length 144218;
  Best Local Similarity   91.7%;  Pred. No. 1.1e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              |||| || ||||||||||||||||
Db     128480 CTCAACCACGTCACCTCACCACAG 128457


RESULT 13
AC116432/c
LOCUS       AC116432              192018 bp    DNA     linear   HTG 06-SEP-2002
DEFINITION  Papio anubis clone RP41-41N12, WORKING DRAFT SEQUENCE, 4 ordered
            pieces.
ACCESSION   AC116432
VERSION     AC116432.2  GI:22748392
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 192018)
  AUTHORS   Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
            Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
            Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,
            Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
            Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
            McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
            Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schueler,M.G., Sison,C.,
            Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
            Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 192018)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-2002) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
REFERENCE   3  (bases 1 to 192018)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-SEP-2002) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     On Sep 6, 2002 this sequence version replaced gi:19774495.
            -------------- Genome Center
                 Center: NIH Intramural Sequencing Center
                 Center code: NISC
                 Web site: http://www.nisc.nih.gov
                 Contact: nisc_zoo@nhgri.nih.gov
            -------------- Project Information
                 Center project name: cyf
                 Center clone name: 041N12

            The sequence data in this record represents an 'enhanced'
            version of a Phase 2 submission. Specifically, the indicated
            order and orientation of each sequence contig has been
            established using one or more of the following: read-pair
            data from individual subclones, overlaps with neighboring
            clones, alignment with available reference sequence (e.g.,
            human), and/or confirmation by PCR testing. In addition,
            the sequence assembly is based on at least 8X average
            coverage in Q20 bases and has been reviewed to rule out
            gross misassemblies, the low-quality ends of sequence
            contigs have been trimmed away, and each base is associated
            with a Phrap-derived quality score.
            -------------- Summary Statistics
                 Sequencing vector: plasmid; n/a; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990319
                 Consensus quality: 191197 bases at least Q40
                 Consensus quality: 191446 bases at least Q30
                 Consensus quality: 191636 bases at least Q20
                 Insert size: 175000; agarose-fp
                 Insert size: 191718; sum-of-contigs
                 Quality coverage: 11.36x in Q20 bases; agarose-fp
                 Quality coverage: 10.37x in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    52603: contig of 52603 bp in length
            *    52604    52703: gap of unknown length
            *    52704   146318: contig of 93615 bp in length
            *   146319   146418: gap of unknown length
            *   146419   160467: contig of 14049 bp in length
            *   160468   160567: gap of unknown length
            *   160568   192018: contig of 31451 bp in length.
FEATURES             Location/Qualifiers
     source          1. .192018
                     /organism="Papio anubis"
                     /mol_type="genomic DNA"
                     /sub_species="anubis"
                     /db_xref="taxon:9555"
                     /clone="RP41-41N12"
                     /clone_lib="RP41"
     misc_feature    1. .52603
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:left"
     misc_feature    1. .31662
                     /note="clone overlaps with GenBank Accession Number
                     AC116431 clone RP41-396O11 (center project name cyd)"
     gap             52604. .52703
                     /estimated_length=unknown
     misc_feature    52704. .146318
                     /note="assembly_fragment"
     misc_feature    80570. .192018
                     /note="clone overlaps with GenBank Accession Number
                     AC116430 clone RP41-348B20 (center project name cyg)"
     gap             146319. .146418
                     /estimated_length=unknown
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```
     misc_feature    146419. .160467
                     /note="assembly_fragment"
     gap             160468. .160567
                     /estimated_length=unknown
     misc_feature    160568. .192018
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 12;  Length 192018;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              |||| || ||||||||||||||||
Db      63324 CTCAACCACGTCACCTCACCACAG 63301


RESULT 14
AC147059/c
LOCUS       AC147059              193301 bp    DNA     linear   HTG 09-JAN-2004
DEFINITION  Pan troglodytes chromosome 7 clone RP43-155J4, WORKING DRAFT
            SEQUENCE, 5 unordered pieces.
ACCESSION   AC147059
VERSION     AC147059.2  GI:40786700
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 193301)
  AUTHORS   Wilson,R.K.
  TITLE     The sequence of Pan troglodytes clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 193301)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444
            Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE   3  (bases 1 to 193301)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2004) Genetics, Genome Sequencing Center, 4444
            Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT     On Jan 9, 2004 this sequence version replaced gi:38154089.

            ---------- Genome Center ----------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu
            Contact: submissions@watson.wustl.edu
            ---------- Project Information ----------
            Center project name: C_PT155J04
            ----------
            ---------- Summary Statistics  ----------
            Sequencing vector: M13; %
            Sequencing vector: plasmid; %
            Chemistry: Dye-primer ET; % of reads
            Chemistry: Dye-terminator Big Dye; % of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 192031 bases at least Q40
            Consensus quality: 192348 bases at least Q30
            Consensus quality: 192477 bases at least Q20
            ----------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 5 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1414: contig of 1414 bp in length
            *     1415     1514: gap of unknown length
            *     1515     2808: contig of 1294 bp in length
            *     2809     2908: gap of unknown length
            *     2909     4218: contig of 1310 bp in length
            *     4219     4318: gap of unknown length
            *     4319    62250: contig of 57932 bp in length
            *    62251    62350: gap of unknown length
            *    62351   193301: contig of 130951 bp in length.
FEATURES             Location/Qualifiers
     source          1. .193301
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /chromosome="7"
                     /clone="RP43-155J4"
     misc_feature    1. .1414
                     /note="assembly_name:Contig8"
     gap             1415. .1514
                     /estimated_length=unknown
     misc_feature    1515. .2808
                     /note="assembly_name:Contig15"
     gap             2809. .2908
                     /estimated_length=unknown
     misc_feature    2909. .4218
                     /note="assembly_name:Contig22"
     gap             4219. .4318
                     /estimated_length=unknown
     misc_feature    4319. .62250
                     /note="assembly_name:Contig32"
     gap             62251. .62350
                     /estimated_length=unknown
     misc_feature    62351. .193301
                     /note="assembly_name:Contig33"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 12;  Length 193301;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              |||||||||||| || ||||||||
Db      10856 CTCAGCCTCGTCTCCCCACCACAG 10833


RESULT 15
CP000249_24/c
WPCOMMENT
  Sequence split into 55 fragments  LOCUS CP000249 Accession CP000249
     Fragment Name      Begin     End
     CP000249_00            1    110000
     CP000249_01       100001    210000
     CP000249_02       200001    310000
     CP000249_03       300001    410000
     CP000249_04       400001    510000
     CP000249_05       500001    610000
     CP000249_06       600001    710000
     CP000249_07       700001    810000
     CP000249_08       800001    910000
     CP000249_09       900001   1010000
     CP000249_10      1000001   1110000
     CP000249_11      1100001   1210000
     CP000249_12      1200001   1310000
     CP000249_13      1300001   1410000
     CP000249_14      1400001   1510000
     CP000249_15      1500001   1610000
     CP000249_16      1600001   1710000
     CP000249_17      1700001   1810000
     CP000249_18      1800001   1910000
     CP000249_19      1900001   2010000
     CP000249_20      2000001   2110000
     CP000249_21      2100001   2210000
```

CP000249_22	2200001	2310000
CP000249_23	2300001	2410000
CP000249_24	2400001	2510000
CP000249_25	2500001	2610000
CP000249_26	2600001	2710000
CP000249_27	2700001	2810000
CP000249_28	2800001	2910000
CP000249_29	2900001	3010000
CP000249_30	3000001	3110000
CP000249_31	3100001	3210000
CP000249_32	3200001	3310000
CP000249_33	3300001	3410000
CP000249_34	3400001	3510000
CP000249_35	3500001	3610000
CP000249_36	3600001	3710000
CP000249_37	3700001	3810000
CP000249_38	3800001	3910000
CP000249_39	3900001	4010000
CP000249_40	4000001	4110000
CP000249_41	4100001	4210000
CP000249_42	4200001	4310000
CP000249_43	4300001	4410000
CP000249_44	4400001	4510000
CP000249_45	4500001	4610000
CP000249_46	4600001	4710000
CP000249_47	4700001	4810000
CP000249_48	4800001	4910000
CP000249_49	4900001	5010000
CP000249_50	5000001	5110000
CP000249_51	5100001	5210000
CP000249_52	5200001	5310000
CP000249_53	5300001	5410000
CP000249_54	5400001	5433628

Continuation (25 of 55) of CP000249 from base 2400001 (CP000249 Frankia sp. CcI3, comple

Query Match 77.7%; Score 20.2; DB 15; Length 110000;
Best Local Similarity 88.0%; Pred. No. 2.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 GACTCAGCCTCGTCACCTCACCACA 25
              |||||| || |||| ||||||||||
Db      99406 GACTCATCCGCGTCGCCTCACCACA 99382
```

Search completed: July 1, 2006, 00:03:32
Job time : 961.45 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:13:35 ; Search time 3510 Seconds
(without alignments)
414.217 Million cell updates/sec

Title: US-10-615-497-11
Perfect score: 26
Sequence: 1 gactcagcctcgtcacctcaccacag 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	24	92.3	954	3	BQ959322	BQ959322 AGENCOURT
c	2	21.2	81.5	676	13	CW864103	CW864103 she2h2-49
	3	21	80.8	206	2	BG982279	BG982279 CM4-CN008
c	4	20.8	80.0	539	3	BW141121	BW141121 BW141121
c	5	20.8	80.0	564	7	AV901364	AV901364 AV901364
c	6	20.8	80.0	594	7	AV853149	AV853149 AV853149
c	7	20.8	80.0	650	3	BW148997	BW148997 BW148997
c	8	20.8	80.0	667	3	BW374508	BW374508 BW374508
c	9	20.8	80.0	667	7	AV846431	AV846431 AV846431
c	10	20.8	80.0	680	3	BW137614	BW137614 BW137614
c	11	20.8	80.0	688	3	BW133937	BW133937 BW133937
c	12	20.8	80.0	694	3	BW025072	BW025072 BW025072
c	13	20.8	80.0	696	3	BW067587	BW067587 BW067587
c	14	20.8	80.0	696	3	BW096416	BW096416 BW096416
c	15	20.8	80.0	698	3	BW016132	BW016132 BW016132
c	16	20.8	80.0	703	7	AV875308	AV875308 AV875308
c	17	20.8	80.0	704	3	BW084880	BW084880 BW084880
c	18	20.8	80.0	705	3	BW082592	BW082592 BW082592
c	19	20.8	80.0	711	7	AV862371	AV862371 AV862371
c	20	20.8	80.0	713	3	BW386286	BW386286 BW386286
c	21	20.8	80.0	761	3	BW452349	BW452349 BW452349
c	22	20.8	80.0	764	3	BW408374	BW408374 BW408374
	23	20.2	77.7	885	5	CF585514	CF585514 AGENCOURT
c	24	19.8	76.2	335	10	DV717210	DV717210 RVL7676 W
c	25	19.8	76.2	386	4	CB806418	CB806418 AMGNNUC:S
c	26	19.8	76.2	418	4	CB765741	CB765741 AMGNNUC:S
	27	19.8	76.2	420	7	AW522167	AW522167 UI-R-BO0-
	28	19.8	76.2	441	1	AI715193	AI715193 UI-R-Y0-a
c	29	19.8	76.2	445	4	CB744414	CB744414 AMGNNUC:S
c	30	19.8	76.2	463	3	BW075866	BW075866 BW075866
	31	19.8	76.2	480	3	BP481037	BP481037 BP481037
	32	19.8	76.2	500	3	BP472760	BP472760 BP472760
	33	19.8	76.2	525	2	BM383000	BM383000 UI-R-DS0-
	34	19.8	76.2	525	3	BP467335	BP467335 BP467335
	35	19.8	76.2	545	1	AI575423	AI575423 UI-R-Y0-v
c	36	19.8	76.2	549	1	AJ651004	AJ651004 AJ651004
c	37	19.8	76.2	561	4	CB609623	CB609623 AMGNNUC:S
c	38	19.8	76.2	573	4	CB615039	CB615039 AMGNNUC:S
c	39	19.8	76.2	602	4	CB582120	CB582120 AMGNNUC:S
c	40	19.8	76.2	649	8	CX177856	CX177856 D11_45-40
	41	19.8	76.2	678	8	CV111238	CV111238 AGENCOURT
c	42	19.8	76.2	695	3	BW163317	BW163317 BW163317
c	43	19.8	76.2	696	8	CO561280	CO561280 AGENCOURT
	44	19.8	76.2	741	8	CV797135	CV797135 UI-R-EA0-
c	45	19.8	76.2	821	8	CO555268	CO555268 AGENCOURT

ALIGNMENTS

RESULT 1
BQ959322/c
LOCUS BQ959322 954 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8922624 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6470087 5', mRNA sequence.
ACCESSION BQ959322
VERSION BQ959322.1 GI:22374800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 954)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14000 row: d column: 24
High quality sequence stop: 694.
FEATURES Location/Qualifiers
source 1. .954
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6470087"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "
ORIGIN

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  Query Match             92.3%;  Score 24;  DB 3;  Length 954;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db        329 CTCAGCCTCGTCACCTCACCACAG 306


RESULT 2
CW864103/c
LOCUS       CW864103                676 bp    DNA     linear   GSS 12-FEB-2005
DEFINITION  she2h2-49.b_068.ab1 Whole-genome shotgun library of the elephant
            shark (aka elephant fish) Callorhinchus milii genomic, genomic
            survey sequence.
ACCESSION   CW864103
VERSION     CW864103.1  GI:59687689
KEYWORDS    GSS.
SOURCE      Callorhinchus milii (elephantfish)
  ORGANISM  Callorhinchus milii
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
            Holocephali; Chimaeriformes; Callorhinchidae; Callorhinchus.
REFERENCE   1  (bases 1 to 676)
  AUTHORS   Venkatesh,B., Tay,A., Dandona,N., Patil,J.G. and Brenner,S.
  TITLE     A compact cartilaginous fish model genome
  JOURNAL   Curr. Biol. 15 (3), R82-R83 (2005)
   PUBMED   15694293
COMMENT     Contact: Venkatesh B
            Molecular Genetics Lab
            Institute of Molecular and Cell Biology
            61 Biopolis Drive, Singapore 138673
            Tel: 65 6586 9571
            Fax: 65 6779 1117
            Email: mcbbv@imcb.a-star.edu.sg
            Whole-genome shotgun sequences of the elephant shark (aka elephant
            fish)
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .676
                     /organism="Callorhinchus milii"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7868"
                     /sex="Male"
                     /tissue_type="Testis"
                     /clone_lib="Whole-genome shotgun library of the elephant
                     shark (aka elephant fish)"
ORIGIN

  Query Match             81.5%;  Score 21.2;  DB 13;  Length 676;
  Best Local Similarity   88.5%;  Pred. No. 3.8e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| ||||| | ||||||||||||||
Db        425 GACACAGCCGCTTCACCTCACCACAG 400


RESULT 3
BG982279
LOCUS       BG982279                206 bp    mRNA    linear   EST 12-JUN-2001
DEFINITION  CM4-CN0089-130201-723-a06 CN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG982279
VERSION     BG982279.1  GI:14385014
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 206)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM4&t2=CM4-CN0089-
            130201-723-a06&t3=2001-02-13&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 10
            High quality sequence stop: 206.
FEATURES             Location/Qualifiers
     source          1. .206
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="CN0089"
                     /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             80.8%;  Score 21;  DB 2;  Length 206;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AGCCTCGTCACCTCACCACAG 26
              |||||||||||||||||||||
Db         37 AGCCTCGTCACCTCACCACAG 57


RESULT 4
BW141121/c
LOCUS       BW141121                539 bp    mRNA    linear   EST 01-JUN-2005
DEFINITION  BW141121 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone rcign058c12 3', mRNA sequence.
ACCESSION   BW141121
VERSION     BW141121.1  GI:24498346
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Ciona intestinalis"
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                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcign058c12"
                     /tissue_type="whole animal"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 539;
  Best Local Similarity   91.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        385 GACACAGCCTCGTCATCTCACCAC 362


RESULT 5
AV901364/c
LOCUS       AV901364                564 bp    mRNA    linear   EST 09-NOV-2001
DEFINITION  AV901364 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone rciad47m05 3', mRNA sequence.
ACCESSION   AV901364
VERSION     AV901364.1  GI:16890462
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .564
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rciad47m05"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 7;  Length 564;
  Best Local Similarity   91.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        397 GACACAGCCTCGTCATCTCACCAC 374


RESULT 6
AV853149/c
LOCUS       AV853149                594 bp    mRNA    linear   EST 08-NOV-2001
DEFINITION  AV853149 Nori Satoh unpublished cDNA library, egg Ciona
            intestinalis cDNA clone rcieg17c15 3', mRNA sequence.
ACCESSION   AV853149
VERSION     AV853149.1  GI:16839000
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcieg17c15"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /clone_lib="Nori Satoh unpublished cDNA library, egg"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 7;  Length 594;
  Best Local Similarity   91.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        394 GACACAGCCTCGTCATCTCACCAC 371


RESULT 7
BW148997/c
LOCUS       BW148997                650 bp    mRNA    linear   EST 01-JUN-2005
DEFINITION  BW148997 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone rcign081p18 3', mRNA sequence.
ACCESSION   BW148997
VERSION     BW148997.1  GI:24506222
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 650)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .650
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcign081p18"
                     /tissue_type="whole animal"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 650;
  Best Local Similarity   91.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
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Db        384 GACACAGCCTCGTCATCTCACCAC 361


RESULT 8
BW374508/c
LOCUS       BW374508                667 bp    mRNA    linear   EST 28-MAY-2004
DEFINITION  BW374508 Yutaka Satou unpublished cDNA library, adult digestive
            gland Ciona intestinalis cDNA clone cidg804n20 3', mRNA sequence.
ACCESSION   BW374508
VERSION     BW374508.1  GI:47790336
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Yutaka Satou
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4095
            Fax: 81-75-705-1113
            Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cidg804n20"
                     /tissue_type="digestive gland"
                     /dev_stage="adult"
                     /clone_lib="Yutaka Satou unpublished cDNA library, adult
                     digestive gland"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 667;
  Best Local Similarity   91.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        357 GACACAGCCTCGTCATCTCACCAC 334


RESULT 9
AV846431/c
LOCUS       AV846431                667 bp    mRNA    linear   EST 26-MAY-2005
DEFINITION  AV846431 Nori Satoh unpublished cDNA library, cleavage stage embryo
            Ciona intestinalis cDNA clone rcicl16g02 3', mRNA sequence.
ACCESSION   AV846431
VERSION     AV846431.1  GI:16825815
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcicl16g02"
                     /tissue_type="whole animal"
                     /dev_stage="cleaving embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, cleavage
                     stage embryo"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 7;  Length 667;
  Best Local Similarity   91.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        402 GACACAGCCTCGTCATCTCACCAC 379


RESULT 10
BW137614/c
LOCUS       BW137614                680 bp    mRNA    linear   EST 01-JUN-2005
DEFINITION  BW137614 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone rcign047i23 3', mRNA sequence.
ACCESSION   BW137614
VERSION     BW137614.1  GI:24494013
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcign047i23"
                     /tissue_type="whole animal"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 680;
  Best Local Similarity   91.7%;  Pred. No. 5.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        377 GACACAGCCTCGTCATCTCACCAC 354


RESULT 11
BW133937/c
LOCUS       BW133937                688 bp    mRNA    linear   EST 01-JUN-2005
DEFINITION  BW133937 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone rcign035e22 3', mRNA sequence.
ACCESSION   BW133937
VERSION     BW133937.1  GI:24490336
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
```

```
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .688
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcign035e22"
                     /tissue_type="whole animal"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 688;
  Best Local Similarity   91.7%;  Pred. No. 5.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        385 GACACAGCCTCGTCATCTCACCAC 362


RESULT 12
BW025072/c
LOCUS       BW025072                694 bp    mRNA    linear   EST 13-OCT-2002
DEFINITION  BW025072 Nori Satoh unpublished cDNA library, blood cells Ciona
            intestinalis cDNA clone rcibd007j10 3', mRNA sequence.
ACCESSION   BW025072
VERSION     BW025072.1  GI:23940879
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 694)
  AUTHORS   Satou,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and
            Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .694
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcibd007j10"
                     /tissue_type="blood cells"
                     /clone_lib="Nori Satoh unpublished cDNA library, blood
                     cells"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 694;
  Best Local Similarity   91.7%;  Pred. No. 5.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        382 GACACAGCCTCGTCATCTCACCAC 359


RESULT 13
BW067587/c
LOCUS       BW067587                696 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BW067587 Nori Satoh unpublished cDNA library, cleaving embryo Ciona
            intestinalis cDNA clone rcicl103b23 3', mRNA sequence.
ACCESSION   BW067587
VERSION     BW067587.1  GI:24168999
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .696
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcicl103b23"
                     /tissue_type="whole body"
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                     /clone_lib="Nori Satoh unpublished cDNA library, cleaving
                     embryo"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 696;
  Best Local Similarity   91.7%;  Pred. No. 5.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||||| ||||||||
Db        393 GACACAGCCTCGTCATCTCACCAC 370


RESULT 14
BW096416/c
LOCUS       BW096416                696 bp    mRNA    linear   EST 27-MAY-2005
DEFINITION  BW096416 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
            intestinalis cDNA clone rcitb055m19 3', mRNA sequence.
ACCESSION   BW096416
VERSION     BW096416.1  GI:24310229
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .696
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                     /organism="Ciona intestinalis"
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                     /db_xref="taxon:7719"
                     /clone="rcitb055m19"
                     /tissue_type="whole animal"
                     /dev_stage="tailbud embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, tailbud
                     embryo"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 696;
  Best Local Similarity   91.7%;  Pred. No. 5.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||| ||||||||
Db        383 GACACAGCCTCGTCATCTCACCAC 360


RESULT 15
BW016132/c
LOCUS       BW016132                698 bp    mRNA    linear   EST 13-OCT-2002
DEFINITION  BW016132 Nori Satoh unpublished cDNA library, blood cells Ciona
            intestinalis cDNA clone rcibd055e15 3', mRNA sequence.
ACCESSION   BW016132
VERSION     BW016132.1  GI:23931939
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Satou,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and
            Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcibd055e15"
                     /tissue_type="blood cells"
                     /clone_lib="Nori Satoh unpublished cDNA library, blood
                     cells"
ORIGIN

  Query Match             80.0%;  Score 20.8;  DB 3;  Length 698;
  Best Local Similarity   91.7%;  Pred. No. 5.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              ||| |||||||||| ||||||||
Db        385 GACACAGCCTCGTCATCTCACCAC 362


Search completed: July  1, 2006, 01:17:49
Job time : 3513 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:12:00 ; Search time 221.65 Seconds
(without alignments)
817.859 Million cell updates/sec

Title: US-10-615-497-11
Perfect score: 26
Sequence: 1 gactcagcctcgtcacctcaccacag 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	26	100.0	26	12	ADO03976	Ado03976 Human CYP
	2	24	92.3	6472	6	ABQ72215	Abq72215 Human CYP
	3	24	92.3	6472	6	ABQ72364	Abq72364 Human CYP
	4	24	92.3	9432	6	AAD34213	Aad34213 Human cyt
	5	24	92.3	9432	10	ACA61301	Aca61301 Human cyt
	6	24	92.3	9432	12	ADF83400	Adf83400 Human CYP
	7	24	92.3	9432	12	ADJ78563	Adj78563 Human cyt
	8	24	92.3	9432	12	ADM28891	Adm28891 Human wil
	9	24	92.3	9432	15	AEF35804	Aef35804 Human cyt
	10	24	92.3	9432	15	AEF38201	Aef38201 Human deb
	11	24	92.3	9433	10	ACA61302	Aca61302 Human cyt
	12	24	92.3	9609	14	ADX00827	Adx00827 Human CYP
	13	24	92.3	18000	15	AEF35808	Aef35808 Human cyt
	14	22	84.6	2788	12	ADF83398	Adf83398 Human CYP
c	15	20.2	77.7	181684	11	ACN44374	Acn44374 Human gen
c	16	19.2	73.8	1555	10	ADD47932	Add47932 Rat gene
	17	19.2	73.8	8355	2	AAT35524	Aat35524 Human int
c	18	19	73.1	19	12	ADJ14676	Adj14676 Debrisoqu
c	19	19	73.1	19	12	ADO60778	Ado60778 Human deb
c	20	19	73.1	19	12	ADO60901	Ado60901 Human deb
c	21	19	73.1	19	14	AEC90065	Aec90065 CYP2D6 ge
c	22	19	73.1	19	14	AEC89942	Aec89942 CYP2D6 ge
	23	19	73.1	20	15	AEF38204	Aef38204 Human deb
	24	19	73.1	21	12	ADO03970	Ado03970 Human CYP
c	25	19	73.1	23	12	ADJ14705	Adj14705 Debrisoqu
c	26	19	73.1	23	12	ADJ14788	Adj14788 Debrisoqu
c	27	19	73.1	23	12	ADO60879	Ado60879 Human deb
c	28	19	73.1	23	12	ADO60808	Ado60808 Human deb
c	29	19	73.1	23	14	ADZ71127	Adz71127 Human CYP
c	30	19	73.1	23	14	AEC90043	Aec90043 CYP2D6 ge
c	31	19	73.1	23	14	AEC89972	Aec89972 CYP2D6 ge
c	32	19	73.1	71	12	ADJ14768	Adj14768 Debrisoqu
	33	18.8	72.3	1472	10	ADD71964	Add71964 Human uri
	34	18.8	72.3	1474	10	ADD71965	Add71965 Human uri
	35	18.8	72.3	4063	10	ADD72083	Add72083 Human uri
	36	18.6	71.5	828	10	ADD31014	Add31014 Plant yie
	37	18.6	71.5	828	10	AAD47505	Aad47505 Arabidops
	38	18.6	71.5	828	12	ADI44306	Adi44306 Plant tra
	39	18.6	71.5	1365	13	ADX30143	Adx30143 Plant ful
c	40	18.6	71.5	5524	4	AAH16668	Aah16668 Human cDN
	41	18.6	71.5	54303	13	ABD32752	Abd32752 Mouse can
	42	18.6	71.5	58326	12	ADO48537	Ado48537 Human man
	43	18.6	71.5	68200	14	ADX80722	Adx80722 Human man
c	44	18.2	70.0	1197	10	ADB53886	Adb53886 Primary r
c	45	18.2	70.0	1197	13	ADV41786	Adv41786 Rat cardi

ALIGNMENTS

RESULT 1
ADO03976
ID ADO03976 standard; DNA; 26 BP.
XX
AC ADO03976;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human CYP2D6 gene polymorphism detecting PCR primer, SNP13.
XX
KW Cytochrome P450 2D6; CYP2D6; polymorphism detection;
KW single nucleotide polymorphism; respiratory system; cystic fibrosis;
KW asthma; bronchitis; adult respiratory distress syndrome;
KW digestive system; cancer; inflammatory bowel disease; Crohn's disease;
KW pancreatitis; skeletal system; rheumatoid arthritis; osteoporosis;
KW spinal muscular atrophy; autoimmune disease; multiple sclerosis;
KW psoriasis; insulin dependent diabetes mellitus;
KW systemic lupus erythematosus; autoimmune haemolytic anaemia;
KW neurological disorder; Alzheimer's disease; Parkinson's disease;
KW schizophrenia; leukaemia; aging; human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2004091909-A1.
XX
PD 13-MAY-2004.
XX
PF 07-JUL-2003; 2003US-00615497.
XX
PR 05-JUL-2002; 2002US-0393967P.
PR 16-JUL-2002; 2002US-0396618P.
XX
PA (HUAN/) HUANG D H.
XX
PI Huang DH;
XX
DR WPI; 2004-374942/35.
XX
PT Identifying pre-selected polymorphisms present in cytochrome P450 2D6
PT gene sequences in samples, by generating a labeled nucleic acid and
PT relating labeled nucleic acid to identity of polymorphism.

```
XX
PS   Claim 33; SEQ ID NO 11; 27pp; English.
XX
CC   The invention relates to methods for identifying several pre-selected
CC   polymorphisms present in cytochrome P450 2D6 (CYP2D6) gene. The method is
CC   useful for identifying pre-selected polymorphisms present in cytochrome
CC   P450 2D6 gene sequence, e.g., duplication, deletion, inversion,
CC   insertion, translocation, polymorphism resulting in aberrant RNA splicing
CC   and a single nucleotide polymorphism. It is useful for selecting a
CC   therapeutic drug or its prodrug to treat a subject suffering from a
CC   disease or disorder that involves the respiratory system (cystic
CC   fibrosis, asthma, bronchitis and adult respiratory distress syndrome),
CC   digestive system (cancers, inflammatory bowel disease, Crohn's disease
CC   and pancreatitis), skeletal system (rheumatoid arthritis, osteoporosis
CC   and spinal muscular atrophy), autoimmune disease (multiple sclerosis,
CC   psoriasis, insulin dependent diabetes mellitus, systemic lupus
CC   erythematosus and autoimmune haemolytic anaemia), neurological disorders
CC   (Alzheimer's disease, Parkinson's disease and schizophrenia), various
CC   leukaemias and aging. The present sequence is a PCR primer used for
CC   detecting human CYP2D6 gene polymorphism. This sequence is used to
CC   illustrate the method of the invention.
XX
SQ   Sequence 26 BP; 6 A; 12 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 26;  DB 12;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.36;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||||
Db          1 GACTCAGCCTCGTCACCTCACCACAG 26


RESULT 2
ABQ72215
ID   ABQ72215 standard; DNA; 6472 BP.
XX
AC   ABQ72215;
XX
DT   02-SEP-2002  (first entry)
XX
DE   Human CYP2D6 gene, SEQ ID NO:1 version #1.
XX
KW   Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme;
KW   chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase;
KW   antiarrhythmic; arrhythmia; adrenoreceptor antagonist; hypertension;
KW   tricyclic antidepressant; procainamide; drug induced lupus syndrome;
KW   environmentally linked disease; Parkinsons's disease; haplotyping;
KW   genotyping; haplotype; genetic variant; single nucleotide polymorphism;
KW   SNP; drug screening; drug discovery; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /label= PS1
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
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FT   variation       replace(678, C)
FT                   /*tag=  b
FT                   /label= PS2
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification"
FT   variation       replace(769, C)
FT                   /*tag=  c
FT                   /label= PS3
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as S in the specification"
FT   variation       replace(776, G)
FT                   /*tag=  d
FT                   /label= PS4
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as R in the specification"
FT   variation       replace(825, A)
FT                   /*tag=  e
FT                   /label= PS5
FT                   /note= "Known single nucleotide polymorphism (SNP); given
FT                   as R in the specification"
FT   variation       replace(915, C)
FT                   /*tag=  f
FT                   /label= PS6
FT                   /note= "Novel single nucleotide polymorphism (SNP); given
FT                   as Y in the specification"
FT   CDS             1001. .5217
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FT   exon            1001. .1180
FT                   /*tag=  h
FT                   /number= 1
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FT                   /*tag=  i
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FT                   substitution V7M"
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FT                   /label= PS8
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FT                   /label= PS9
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FT                   substitution R88H"
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FT                   /*tag=  q
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FT                   as M in the specification; causes the amino acid
FT                   substitution L91M"
FT   variation       replace(1984, G)
FT                   /*tag=  r
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FT                   as R in the specification; causes the amino acid
FT                   substitution H94R"
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FT                      /label= PS19
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FT                      substitution I109V"
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FT                      substitution W128R"
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FT                      /label= PS29
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  Query Match             92.3%;  Score 24;  DB 6;  Length 6472;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       5814 CTCAGCCTCGTCACCTCACCACAG 5837


RESULT 3
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ID   ABQ72364 standard; DNA; 6472 BP.
XX
AC   ABQ72364;
XX
DT   02-SEP-2002. (first entry)
XX
DE   Human CYP2D6 gene, SEQ ID NO:1 version #2.
XX
KW   Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme;
KW   chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase;
KW   antiarrhythmic; arrhythmia; adrenoreceptor antagonist; hypertension;
KW   tricyclic antidepressant; procainamide; drug induced lupus syndrome;
KW   environmentally linked disease; Parkinsons's disease; haplotyping;
KW   genotyping; haplotype; genetic variant; single nucleotide polymorphism;
KW   SNP; drug screening; drug discovery; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
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FT                   /label= PS3
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FT   variation       replace(776, G)
FT                   /*tag= d
FT                   /label= PS4
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(825, A)
FT                   /*tag= e
FT                   /label= PS5
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FT   variation       replace(915, C)
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FT   variation       replace(2118, T)
FT                   /*tag= ac
FT                   /label= PS24
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   variation       replace(2170, A)
FT                   /*tag= ad
FT                   /label= PS25
FT                   /note= "Known single nucleotide polymorphism (SNP)"
FT   variation       replace(2179, C)
FT                   /*tag= ae
FT                   /label= PS26
FT                   /note= "Novel single nucleotide polymorphism (SNP)"
FT   exon            2606. .2758
FT                   /*tag= af
FT                   /number= 3
FT   variation       replace(2611, A)
FT                   /*tag= ag
FT                   /label= PS27
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution F120I"
FT   variation       replace(2635, C)
FT                   /*tag= ah
FT                   /label= PS28
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution W128R"
FT   variation       replace(2659, A)
FT                   /*tag= ai
FT                   /label= PS29
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   together with PS30 causes the amino acid substitution
FT                   V136I"
FT   variation       replace(2661, C)
FT                   /*tag= aj
FT                   /label= PS30
FT                   /note= "Known single nucleotide polymorphism (SNP);
FT                   together with PS29 causes the amino acid substitution
FT                   V136I"
FT   variation       replace(2704, G)
FT                   /*tag= ak
FT                   /label= PS31
FT                   /note= "Known single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution Q151E"
FT   variation       replace(2716, A)
FT                   /*tag= al
FT                   /label= PS32
FT                   /note= "Novel single nucleotide polymorphism (SNP);
FT                   causes the amino acid substitution E155K"
FT   intron          2759. .2846
FT                   /*tag= am
FT                   /number= 3
FT   variation       replace(2846, A)
FT                   /*tag= an
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```
FT                   /label= PS33
FT                   /note= "Known single nucleotide polymorphism (SNP)"
FT   exon            2847. .3007
FT                   /*tag=  ao
FT                   /number= 4
FT   intron          3008. .3440
FT                   /*tag=  ap
FT                   /number= 4
FT   variation       replace(3292, A)

  Query Match             92.3%;  Score 24;  DB 6;  Length 6472;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       5814 CTCAGCCTCGTCACCTCACCACAG 5837


RESULT 4
AAD34213
ID   AAD34213 standard; DNA; 9432 BP.
XX
AC   AAD34213;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human cytochrome P450 2D6 (CYP2D6) gene.
XX
KW   Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
KW   ligase-based sequenced determination; drug metabolism; chromosome 22;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218638-A2.
XX
PD   07-MAR-2002.
XX
PF   27-AUG-2001; 2001WO-IB001544.
XX
PR   30-AUG-2000; 2000GB-00021286.
XX
PA   (GEMI-) GEMINI GENOMICS PLC.
XX
PI   Risinger C,  Andersson MK,  Lewander T,  Oliasson E;
XX
DR   WPI; 2002-329785/36.
XX
PT   New sequence determination oligonucleotides, useful for detecting
PT   polymorphic sites in a 5' flanking region of a CYP2D6 gene, as
PT   hybridization probes, as components of diagnostic assays, or in ligase-
PT   based sequence determination.
XX
PS   Example 3; Fig 1; 63pp; English.
XX
CC   The invention relates to sequence determination oligonucleotides for
CC   detecting polymorphic sites in a 5' flanking region of cytochrome P450
CC   2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many
CC   different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The
CC   oligonucleotides may be used as in situ hybridisation probes, in ligase-
CC   based sequenced determination, as components of diagnostic assays, as
CC   probes in sequence determination methods based on mismatches, as
CC   hybridisation-based diagnostic assays, and as components of diagnostic
CC   microarray. CYP2D6 is useful to predict variations in an individual's
CC   ability to metabolise certain drugs. The present sequence is human CYP2D6
CC   gene
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 24;  DB 6;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 5
ACA61301
ID   ACA61301 standard; DNA; 9432 BP.
XX
AC   ACA61301;
XX
DT   16-JUL-2003  (first entry)
XX
DE   Human cytochrome p450 gene CYP2D6, wild-type.
XX
KW   Human; ds; gene; cytochrome P450; CYP2D6; chromosome 22; SNP;
KW   single nucleotide polymorphism; drug metabolism; cardiovascular disorder;
KW   psychiatric disorder; drug sensitivity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(226. .227,ATT)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(971,G)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1111,T)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1726,C)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1846,A)
FT                   /*tag=  f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1846,G)
FT                   /*tag=  e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(2064,A)
FT                   /*tag=  g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3023,A)
FT                   /*tag=  h
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5799,C)
FT                   /*tag=  i
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5816,TA)
FT                   /*tag=  j
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1281755-A2.
XX
PD   05-FEB-2003.
XX
PF   16-JUL-2002; 2002EP-00254972.
XX
PR   31-JUL-2001; 2001US-0309111P.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Milos PM,  Webb SM;
XX
DR   WPI; 2003-373769/36.
XX
PT   New cytochrome P450 2D6 gene variants and polypeptides, useful for
PT   determining if a subject has or is at risk of developing a drug
PT   sensitivity condition or disorder that is associated with an aberrant
PT   CYP2D6 activity.
XX
```

```
PS   Claim 1; Fig 2; 88pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising a cytochrome
CC   P450 2D6 gene variant, e.g. G5799C or C5816AT (referring to the genomic
CC   sequence or the same variant nucleotide in the corresponding cDNA
CC   sequences). Also included are probes, primers (allele specific
CC   oligonucleotides) and arrays used to detect and or amplify the CYP2D6
CC   gene polymorphic regions, the variant polypeptides, antibodies which are
CC   capable of distinguishing between the variant and wild-type polypeptides,
CC   determining whether a subject has a genetic deficiency for metabolising a
CC   drug, evaluating therapy with a drug metabolised by P450 CYP2D6 and
CC   determining whether an individual is susceptible to being a poor
CC   metaboliser of drugs. The DNA probe is useful for hybrisiding to a
CC   variant form of the CYP2D6 gene. The primer is useful for amplifying the
CC   C5816TA allelic variant. The allele specific nucleotide is useful for the
CC   detection of the C5816TA allelic variant. The methods are useful for
CC   determining whether a subject has a genetic deficiency for metabolising a
CC   drug, evaluating therapy with a drug metabolised by P450 CYP2D6, and
CC   determining if an individual is susceptible to being a poor metaboliser
CC   of drugs. The nucleic acids are useful as probes or primers for
CC   determining whether a subject has a genetic deficiency for metabolising
CC   drugs that are substrates of P450 CYP2D6. The methods are useful for
CC   determining if a subject has or is at risk of developing a drug
CC   sensitivity condition or disorder that is associated with an aberrant
CC   CYP2D6 activity, e.g. an aberrant level of a CYP2D6 protein or an
CC   aberrant CYP2D6 bioactivity. The methods are also useful in selecting the
CC   appropriate drugs or determining the course of treatment to administer to
CC   a subject to treat cardiovascular or psychiatric disorders, or for
CC   treating a subject with a drug sensitivity or disorder associated with a
CC   specific allelic variant of a polymorphic region of the CYP2D6 gene. The
CC   antibodies are useful for monitoring CYP2D6 protein levels in an
CC   individual for determining whether a subject has a disease or conditions
CC   associated with an aberrant CYP2D6 protein level. The gene is located on
CC   human chromosome 22. The present sequence is the wild-type CYP2D6 gene
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 24;  DB 10;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 6
ADF83400
ID   ADF83400 standard; DNA; 9432 BP.
XX
AC   ADF83400;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CYP2D6 gene (wild-type).
XX
KW   Human; antiemetic; setrone; cytochrome P450; CYP2D6; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1620. .5836
FT                   /*tag=  b
FT                   /product= "CYP2D6"
FT   exon            1620. .1799
FT                   /*tag=  a
FT   variation       replace(1719,t)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1743,a)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1756. .1757,ttg)
FT                   /*tag=  e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   intron          1800. .2502
FT                   /*tag=  f
FT   variation       replace(2502,c)
FT                   /*tag=  g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   exon            2503. .2674
FT                   /*tag=  h
FT   intron          2675. .3224
FT                   /*tag=  i
FT                   /cons_splice= (5'site:NO, 3'site:YES)
FT   exon            3225. .3377
FT                   /*tag=  j
FT   variation       replace(3325. .3327,gg)
FT                   /*tag=  k
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3377,t)
FT                   /*tag=  l
FT                   /standard_name= "Single nucleotide polymorphism"
FT   intron          3378. .3465
FT                   /*tag=  m
FT   variation       replace(3465,a)
FT                   /*tag=  n
FT                   /standard_name= "Single nucleotide polymorphism"
FT   exon            3466. .3626
FT                   /*tag=  o
FT   intron          3627. .4059
FT                   /*tag=  p
FT   exon            4060. .4236
FT                   /*tag=  q
FT   variation       replace(4167. .4169,cg)
FT                   /*tag=  r
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4231. .4235,ga)
FT                   /*tag=  s
FT                   /standard_name= "Single nucleotide polymorphism"
FT   intron          4237. .4426
FT                   /*tag=  t
FT   exon            4427. .4568
FT                   /*tag=  u
FT   variation       replace(4469,t)
FT                   /*tag=  v
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4554,c)
FT                   /*tag=  w
FT                   /standard_name= "Single nucleotide polymorphism"
FT   intron          4569. .4775
FT                   /*tag=  x
FT   exon            4776. .4963
FT                   /*tag=  y
FT   intron          4964. .5417
FT                   /*tag=  z
FT   exon            5418. .5559
FT                   /*tag=  aa
FT   intron          5560. .5657
FT                   /*tag=  ab
FT   exon            5658. .5836
FT                   /*tag=  ac
FT   variation       replace(5799,c)
FT                   /*tag=  ad
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO2003100091-A1.
XX
PD   04-DEC-2003.
XX
PF   22-MAY-2003; 2003WO-EP005366.
XX
PR   24-MAY-2002; 2002EP-00011491.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
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PI   Brockmoeller HJ;
XX
DR   WPI; 2004-035165/03.
DR   P-PSDB; ADF83401.
DR   GENBANK; GI_181303.
XX
PT   Use of setrones for preparing a pharmaceutical composition for treating
PT   or preventing setrone-treatable diseases in a subject having in its
PT   genome less than three copies of a polynucleotide encoding a functional
PT   CYP2D6 polypeptide.
XX
PS   Disclosure; SEQ ID NO 50; 153pp; English.
XX
CC   The present sequence comprises the human cytochrome P450 CYP2D6 wild-type
CC   gene. CYP2D6 polymorphisms serve as genetic markers for CYP2D6 metabolic
CC   capacity. The invention relates to the use of setrones (antiemetics) for
CC   treating and/or preventing setrone-treatable diseases in a subject having
CC   in its genome fewer than 3 copies of a polynucleotide encoding a
CC   functional CYP2D6 polypeptide. The subject has at least one first variant
CC   allele selected from: CYP2D6*3, CYP2D6*4, CYP2D6*5, CYP2D6*6, CYP2D6*7,
CC   CYP2D6*8, CYP2D6*11, CYP2D6*12 and CYP2D6*15, and preferably has at least
CC   one first variant allele selected from: CYP2D6*1, CYP2D6*2, CYP2D6*9 and
CC   CYP2D6*10. The variant allele results in altered (decreased) expression.
CC   The treatment regimen can be modified according to the genotype of the
CC   subject's CYP2D6 and/or HTR3B gene. Non-responders to antiemetic therapy
CC   can be identified on a pharmacogenetic basis, allowing a suitable therapy
CC   to be selected. The setrone-treatable diseases are postoperative nausea
CC   and/or vomiting, or nausea and/or vomiting secondary to cancer
CC   chemotherapy, radiation therapy, migraine, acetaminophen poisoning,
CC   prostacyclin therapy, and opioid treatment, spinal or epidural opioid-
CC   related pruritus, acute levodopa-induced psychosis, bulimia nervosa,
CC   fibromyalgia, chronic fatigue syndrome, obsessive-compulsive disorders,
CC   schizophrenia, alcoholism, cocaine addiction, opioid withdrawal syndrome,
CC   drug withdrawal phenomena, anxiety disorders, cognitive disturbances,
CC   neuroleptic-induced tardive dyskinesia, Tourette's syndrome, migraine
CC   headache or gastrointestinal motility disorder (all claimed).
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 24;  DB 12;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 7
ADJ78563
ID   ADJ78563 standard; DNA; 9432 BP.
XX
AC   ADJ78563;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human cytochrome P450 isoenzyme 2D6 genomic gene sequence SeqID1.
XX
KW   primer set; variant identification; cytochrome P450 isoenzyme 2D6;
KW   CYP2D6; chromosome 22q13.1; single nucleotide polymorphism; SNP;
KW   low frequency variant; pharmaceutical drugs metabolism; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(1522,T)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1576,GG)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1851,C)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1852,C)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1864,G)
FT                   /*tag=  e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3230,A)
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FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3232,T)
FT                   /*tag=  g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3335,A)
FT                   /*tag=  h
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3542,T)
FT                   /*tag=  i
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3617,C)
FT                   /*tag=  j
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3716,G)
FT                   /*tag=  k
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3922,T)
FT                   /*tag=  l
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4221,T)
FT                   /*tag=  m
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4280,A)
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FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4282,A)
FT                   /*tag=  o
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4379,A)
FT                   /*tag=  p
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4555,C)
FT                   /*tag=  q
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4607,A)
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FT   variation       replace(4820,T)
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FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4854,G)
FT                   /*tag=  t
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4873,C)
FT                   /*tag=  u
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(4878,TGT)
FT                   /*tag=  v
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5003,A)
FT                   /*tag=  w
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5027,C)
FT                   /*tag=  x
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5054,A)
FT                   /*tag=  y
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5409,T)
FT                   /*tag=  z
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5496,A)
FT                   /*tag=  aa
FT                   /standard_name= "Single nucleotide polymorphism"
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FT   variation       replace(5774,T)
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FT   variation       replace(5791,T)
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FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5948,T)
FT                   /*tag= ad
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(6020,T)
FT                   /*tag= ae
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO2004009760-A2.
XX
PD   29-JAN-2004.
XX
PF   09-JUL-2003; 2003WO-US021468.
XX
PR   18-JUL-2002; 2002US-0397010P.
XX
PA   (BIOV-) BIOVENTURES INC.
XX
PI   Dawson EP;
XX
DR   WPI; 2004-132938/13.
DR   P-PSDB; ADJ78565.
XX
PT   New primer set useful for screening a polynucleotide sample to detect and
PT   identify variants in the cytochrome P450 isoenzyme 2D6 gene, and for
PT   detecting low frequency variants affecting pharmaceutical drugs
PT   metabolism.
XX
PS   Claim 11; SEQ ID NO 1; 51pp; English.
XX
CC   This invention relates to novel primer sets that can be used to screen a
CC   polynucleotide sample to detect and identify variants in the cytochrome
CC   P450 isoenzyme 2D6 (CYP2D6) gene. The gene is located on chromosome
CC   22q13.1 and contains several single nucleotide polymorphisms, the details
CC   of which are disclosed in the specification. The methods and compositions
CC   of the present invention are useful for screening a polynucleotide sample
CC   to detect and identify variants in the cytochrome P450 isoenzyme 2D6 gene
CC   and detecting low frequency variants affecting pharmaceutical drugs
CC   metabolism. The present sequence is that of the gene which encodes the
CC   wild-type human cytochrome P450 isoenzyme 2D6 protein and which is
CC   related to the invention. Note: This sequence contains introns, the
CC   number and location of which are not disclosed within the specification.
CC   As well as the featured SNPs, an exon 9 gene conversion is also claimed
CC   in claim 25 of the specification.
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 24;  DB 12;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 8
ADM28891
ID   ADM28891 standard; DNA; 9432 BP.
XX
AC   ADM28891;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human wild-type CYP2D6 gene sequence.
XX
KW   Human; cytochrome P450 isoenzyme 2D6; CYP2D6 isoenzyme;
KW   altered metabolism; chromosome 22q13.1; gene; ds.
XX
OS   Homo sapiens.
XX
PN   US2004072235-A1.
XX
PD   15-APR-2004.
XX
PF   12-NOV-2003; 2003US-00712363.
XX
PR   20-JUL-2001; 2001US-0306675P.
PR   18-JUL-2002; 2002US-00360790.
PR   09-JUL-2003; 2003WO-US021468.
XX
PA   (DAWS/) DAWSON E P.
XX
PI   Dawson EP;
XX
DR   WPI; 2004-328568/30.
DR   P-PSDB; ADM28893.
XX
PT   Novel primer set for screening a polynucleotide sample to detect and
PT   identify variants in the cytochrome P450 isoenzyme 2D6 (CYP2D6) gene in a
PT   polynucleotide sample or a population.
XX
PS   Claim 11; SEQ ID NO 1; 47pp; English.
XX
CC   The present invention relates to a primer set that can be used to screen
CC   a polynucleotide sample to detect and identify variants in the human
CC   cytochrome P450 isoenzyme 2D6 (CYP2D6) gene. Also disclosed is a kit for
CC   the above screening method, a method for predicting the potential for
CC   altered metabolism of a substance, including one or more than one
CC   pharmaceutical drug, by a first individual compared to a second control
CC   individual, where the substance is metabolised by the CYP2D6 isoenzyme, a
CC   purified or isolated variant of wild-type CYP2D6 isoenzyme having one or
CC   more than one of the alterations chosen from F-I at position 120, F-F at
CC   position 120, E-K at position 155, R-R at position 194, F-F at position
CC   219, L-L at position 276, H-H at position 324, R-STOP at position 344, Y-
CC   C at position 355, H-H at position 361, V-FRAMESHIFT at position 363, E-K
CC   at position 418, H-Y at position 478 and F-F at position 483. The primer
CC   set is useful for screening a polynucleotide sample to detect and
CC   identify the presence of one or more than one variant in the CYP2D6 gene
CC   in the sample. The primer set permits amplification from a small
CC   polynucleotide sample of selected portions of the coding portion of the
CC   CYP2D6 gene, or amplification of the entire coding portion of CYP2D6, as
CC   well as the flanking intronic sequences that are relevant to recognition
CC   of splice sites. The primer set further permits the detection of genetic
CC   variants of CYP2D6 without interference from pseudogenes or from
CC   homologous or paralogous genes of non-CYP2D6 cytochrome p450 genes. The
CC   primer set also permits the detection of low frequency variants that
CC   affect pharmaceutical drugs metabolism, thereby decreasing the false
CC   negative rate in variant screening. The present sequence represents human
CC   wild-type CYP2D6 gene. The gene maps to chromosome 22q13.1.
XX
SQ   Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 24;  DB 12;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 9
AEF35804
ID   AEF35804 standard; DNA; 9432 BP.
XX
AC   AEF35804;
XX
DT   23-MAR-2006  (first entry)
XX
DE   Human cytochrome P450 2D6 DNA.
```

XX
KW diagnosis; prophylaxis; hepatitis B infection; hepatitis C infection;
KW hepatitis D infection; drug-induced hepatotoxicity; liver tumor;
KW liver cirrhosis; fibrosis; autoimmune hepatitis;
KW primary biliary cirrhosis; primary sclerosing cholangitis;
KW hemochromatosis; Wilson's disease; alpha-1 antitrypsin deficiency;
KW celiac disease; amyloidosis; gastrointestinal disease;
KW metabolic disorder; inflammation; cardiant; antiinflammatory;
KW hepatotropic; virucide; gastrointestinal-gen.; cns-gen.; metabolic;
KW immunosuppressive; cytostatic; cytochrome P450 2D6; CYP2D6; ds;
KW chromosome-22; gene.
XX
OS Homo sapiens.
XX
PN WO2006003654-A2.
XX
PD 12-JAN-2006.
XX
PF 30-JUN-2005; 2005WO-IL000700.
XX
PR 01-JUL-2004; 2004US-0584179P.
XX
PA (MEDI-) MEDICAL RES FUND TEL AVIV SOURASKY MED.
XX
PI Oren R;
XX
DR WPI; 2006-090428/09.
DR P-PSDB; AEF35802.
DR GENBANK; M33388.
XX
PT Determining if an individual is predisposed to fast progression of liver
PT fibrosis comprises determining a presence or absence of at least one fast
PT progression liver fibrosis-associated genotype.
XX
PS Example 1; SEQ ID NO 6; 105pp; English.
XX
CC The invention relates to a method of determining if an individual is
CC predisposed to fast progression of liver fibrosis or liver cirrhosis
CC comprising determining a presence or absence, in a homozygous or
CC heterozygous form, of at least one fast progression liver fibrosis-
CC associated genotype in the CYP2D6, CYP3A5, CYP2E1, or APO E locus or in
CC neighboring loci of the individual, where the neighboring loci is in
CC linkage disequilibrium with the locus, thus determining if the individual
CC is predisposed to fast progression of liver fibrosis; a kit to carry out
CC the method; a method of preventing fast progression of liver fibrosis in
CC an individual, by upregulating CYP2D6 expression and/or activity; and a
CC method of determining if a drug molecule is capable of inducing or
CC accelerating development of fast progression of liver fibrosis in an
CC individual. The individual is suffering from a hepatitis viral infection
CC caused by hepatitis B, C or D virus, a hepatotoxicity (alcohol- or drug-
CC induced), a liver cancer, a non-alcoholic fatty liver disease (NAFLD), an
CC autoimmune disease (autoimmune hepatitis (AIH), primary biliary cirrhosis
CC (PBC), or primary sclerosing cholangitis (PSC)), a metabolic liver
CC disease (Hemochromatosis, Wilson's disease, or alpha 1 anti trypsin), or
CC a disease with secondary involvement of the liver (celiac disease and/or
CC amyloidosis). The method and kit are useful for determining if an
CC individual is predisposed to fast progression of liver fibrosis. The
CC method and drug are useful for preventing liver cirrhosis and fast
CC progression of liver fibrosis. This sequence is human cytochrome P450 2D6
CC DNA, located on chromosome 22q13.1.
XX
SQ Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 15; Length 9432;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CTCAGCCTCGTCACCTCACCACAG 26
||||||||||||||||||||||||
Db 6433 CTCAGCCTCGTCACCTCACCACAG 6456

RESULT 10

AEF38201
ID AEF38201 standard; DNA; 9432 BP.
XX
AC AEF38201;
XX
DT 23-MAR-2006 (first entry)
XX
DE Human debrisoquine 4-hydroxylase (CYP2D6) gene.
XX
KW Drug metabolism; gene; ds; chromosome-22; cytochrome P450 2D6;
KW debrisoquine 4-hydroxylase; SNP detection; SNP;
KW single nucleotide polymorphism; DNA microarray.
XX
OS Homo sapiens.
XX
PN WO2006002526-A1.
XX
PD 12-JAN-2006.
XX
PF 30-JUN-2005; 2005WO-CA001000.
XX
PR 30-JUN-2004; 2004US-0583605P.
XX
PA (TMBI-) TM BIOSCIENCE CORP.
XX
PI Merante F, Gordon JD, Bortolin S;
XX
DR WPI; 2006-090278/09.
XX
PT Detecting nucleotide variants e.g. 1846G-A at polymorphic sites in gene
PT encoding cytochrome P450-2D6, by amplifying DNA variants, hybridizing
PT tagged extension primers to amplified DNA and to probes, detecting
PT labeled extension products.
XX
PS Disclosure; SEQ ID NO 1; 42pp; English.
XX
CC The invention relates to detecting nucleotide variants chosen from -1584C
CC -G, 1846G-A, 2549A-del at polymorphic sites in the gene encoding
CC cytochrome P450-2D6 (encoding debrisoquine 4-hydroxylase) comprising
CC amplifying regions of DNA containing variants, hybridizing two tagged
CC allele specific extension primers to complementary target sequence in
CC amplified DNA products, extending primers using labeled nucleotides,
CC hybridizing the primers to the probe sequence and detecting the labeled
CC extension products. Also included is a kit (I) for detecting the presence
CC or absence of nucleotide variants at the polymorphic sites comprising a
CC set of at least two tagged allele specific extension primers, where each
CC tagged allele specific extension primer has a 3'-end hybridizing portion
CC including a 3' terminal nucleotide being either complementary to a
CC suspected variant nucleotide or to the corresponding wild-type nucleotide
CC of one of the polymorphic sites and a 5'-end tag portion complementary to
CC a corresponding probe sequence, and where the two tagged allele-specific
CC extension primers are chosen from AEF38210-AEF38235 or a set of PCR
CC amplification primers for amplifying regions of DNA containing the two
CC polymorphic sites, appearing as AEF38202-AEF38209. The method is useful
CC for detecting the presence or absence of nucleotide variants at
CC polymorphic sites in the gene encoding cytochrome P450-2D6, -1584C-G,
CC 100C-G, 1023C-T, 1846G-A, 2549A-del, 2850C-T, 2935A-C, etc. The method is
CC useful for identifying individuals who may have drug metabolism defects
CC (adverse drug reactions) resulting from mutations in the CYP2D6 gene, in
CC high throughput clinical genotyping applications. The method is a novel
CC and a multiplex method for detecting multiple mutations located in the
CC gene encoding CYP2D6. The present sequence represents the Human CYP2d6
CC gene which islocated in chromosome 22q13.1. NOTE: It is not possible to
CC determine the position of the SNPs within this gene since the authors
CC reference the positions to the ATG start codon (e.g. -1584) without
CC indicating where the start codon is within the present sequence.
XX
SQ Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 15; Length 9432;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              |||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 11
ACA61302
ID   ACA61302 standard; DNA; 9433 BP.
XX
AC   ACA61302;
XX
DT   16-JUL-2003  (first entry)
XX
DE   Human cytochrome p450 gene CYP2D6, variant sequence.
XX
KW   Human; ds; gene; cytochrome P450; CYP2D6; chromosome 22; SNP;
KW   single nucleotide polymorphism; drug metabolism; cardiovascular disorder;
KW   psychiatric disorder; drug sensitivity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(226. .227,ATT)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(971,G)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1111,T)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1726,C)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1846,A)
FT                   /*tag=  f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(1846,G)
FT                   /*tag=  e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(2064,A)
FT                   /*tag=  g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(3023,A)
FT                   /*tag=  h
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5799,G)
FT                   /*tag=  i
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(5816. .5817,C)
FT                   /*tag=  j
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1281755-A2.
XX
PD   05-FEB-2003.
XX
PF   16-JUL-2002; 2002EP-00254972.
XX
PR   31-JUL-2001; 2001US-0309111P.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Milos PM,  Webb SM;
XX
DR   WPI; 2003-373769/36.
XX
PT   New cytochrome P450 2D6 gene variants and polypeptides, useful for
PT   determining if a subject has or is at risk of developing a drug
PT   sensitivity condition or disorder that is associated with an aberrant
PT   CYP2D6 activity.
XX
PS   Claim 3; Fig 3; 88pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising a cytochrome
CC   P450 2D6 gene variant, e.g. G5799C or C5816AT (referring to the genomic
CC   sequence or the same variant nucleotide in the corresponding cDNA
CC   sequences). Also included are probes, primers (allele specific
CC   oligonucleotides) and arrays used to detect and or amplify the CYP2D6
CC   gene polymorphic regions, the variant polypeptides, antibodies which are
CC   capable of distinguishing between the variant and wild-type polypeptides,
CC   determining whether a subject has a genetic deficiency for metabolising a
CC   drug, evaluating therapy with a drug metabolised by P450 CYP2D6 and
CC   determining whether an individual is susceptible to being a poor
CC   metaboliser of drugs. The DNA probe is useful for hybrisiding to a
CC   variant form of the CYP2D6 gene. The primer is useful for amplifying the
CC   C5816TA allelic variant. The allele specific nucleotide is useful for the
CC   detection of the C5816TA allelic variant. The methods are useful for
CC   determining whether a subject has a genetic deficiency for metabolising a
CC   drug, evaluating therapy with a drug metabolised by P450 CYP2D6, and
CC   determining if an individual is susceptible to being a poor metaboliser
CC   of drugs. The nucleic acids are useful as probes or primers for
CC   determining whether a subject has a genetic deficiency for metabolising
CC   drugs that are substrates of P450 CYP2D6. The methods are useful for
CC   determining if a subject has or is at risk of developing a drug
CC   sensitivity condition or disorder that is associated with an aberrant
CC   CYP2D6 activity, e.g. an aberrant level of a CYP2D6 protein or an
CC   aberrant CYP2D6 bioactivity. The methods are also useful in selecting the
CC   appropriate drugs or determining the course of treatment to administer to
CC   a subject to treat cardiovascular or psychiatric disorders, or for
CC   treating a subject with a drug sensitivity or disorder associated with a
CC   specific allelic variant of a polymorphic region of the CYP2D6 gene. The
CC   antibodies are useful for monitoring CYP2D6 protein levels in an
CC   individual for determining whether a subject has a disease or conditions
CC   associated with an aberrant CYP2D6 protein level. The gene is located on
CC   human chromosome 22. The present sequence is the variant CYP2D6 gene
CC   carrying both the G5799C and C5816AT variations
XX
SQ   Sequence 9433 BP; 1965 A; 2647 C; 2975 G; 1846 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 24;  DB 10;  Length 9433;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              |||||||||||||||||||||||
Db       6434 CTCAGCCTCGTCACCTCACCACAG 6457


RESULT 12
ADX00827
ID   ADX00827 standard; DNA; 9609 BP.
XX
AC   ADX00827;
XX
DT   21-APR-2005  (first entry)
XX
DE   Human CYP2D6 gene.
XX
KW   DNA purification; SNP detection; cardiovascular-gen.; hypotensive;
KW   neuroleptic; antiarrhythmic; antiemetic; analgesic; anorectic;
KW   tranquilizer; antimanic; antidepressant; allelic variant; CYP2D6 gene;
KW   diagnosis; codeine dependence; depression; hepatitis C virus infection;
KW   psychosis; schizophrenia; Parkinsons disease; forensic; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   allele          replace(4087,A)
FT                   /*tag=  a
FT   allele          replace(4735,A)
FT                   /*tag=  b
FT   allele          replace(4784,A)
FT                   /*tag=  c
XX
PN   US2005032070-A1.
```

XX
PD 10-FEB-2005.
XX
PF 05-AUG-2003; 2003US-00635780.
XX
PR 05-AUG-2003; 2003US-00635780.
XX
PA (RAIM/) RAIMUNDO S.
PA (ZANG/) ZANGER U.
XX
PI Raimundo S, Zanger U;
XX
DR WPI; 2005-161644/17.
XX
PT Novel polynucleotide of molecular variants of Cytochrome P450 2D6
PT (CYP2D6) gene, capable of hybridizing to CYP2D6 gene, is useful in
PT diagnosing disease related to presence of molecular variant of CYP2D6
PT gene.
XX
PS Claim 1; SEQ ID NO 4; 33pp; English.
XX
CC The invention relates to a polynucleotide (I) of molecular variants of
CC CYP2D6 gene, chosen from polynucleotide capable of hybridizing to CYP2D6
CC gene, where the polynucleotide consists of substitution of one or more
CC nucleotides at position corresponding to 4784, 4735 or 4087 of the CYP2D6
CC gene having a fully defined sequence (S1) of 9609 base pairs as given in
CC the specification. (I) is useful for identifying a diagnostic
CC composition, which involves (a) isolating (I) from several subgroups of
CC individuals, where one subgroup has no prevalence for CYP2D6 associated
CC disease, and one or more further subgroup(s) do have prevalence for a
CC CYP2D6 associated disease, and (b) identifying a single nucleotide
CC polymorphism by comparing the nucleic acid sequence of the polynucleotide
CC or the gene of one subgroup having no prevalence for a CYP2D6 associated
CC disease, with one or more further subgroup(s) having a prevalence for a
CC CYP2D6 associated disease. (I) is useful for diagnosing a disease related
CC to the presence of a molecular variant of a CYP2D6 gene or susceptibility
CC to such a disorder, which involves determining the presence of (I) in a
CC sample from a subject. (I) is useful for diagnosing whether a subject has
CC EM, IM or PM phenotype, and for determining whether an individual is at
CC risk for a toxic reaction, non-response, insufficient response, or
CC reduced metabolic activity of CYP2D6 to treatment with a CYP2D6
CC substrate. (I) is useful in selecting a subject suffering from a CYP2D6
CC substrate treatable disease for treatment with the substrate, and in
CC treating a subject suffering from a CYP2D6 substrate treatable disease.
CC (I) is useful for detecting variant polynucleotide of CYP2D6 gene in a
CC sample, which involves contacting (I) with the sample under conditions
CC allowing interaction of variant of CYP2D6 gene with several immobilized
CC targets on (I), and determining the binding of the polynucleotide or the
CC gene to the immobilized targets on (I). (I) is useful for diagnosing a
CC disease, which involves binding of the variant polynucleotide of CYP2D6
CC gene or the gene to the immobilized targets on (IV), where the binding
CC indicates the presence or the absence of the disease or a prevalence for
CC the disease. The disease is codeine dependence, depression, hepatitis C,
CC psychosis, schizophrenia or Parkinson's disease. (I) is useful for
CC diagnosing an altered activity of the CYP2D6 enzyme, and for diagnosing a
CC polynucleotide associated with IM phenotype of CYP2D6. (I) is useful in
CC diagnosing individual's genetic constitution of the CYP2D6 status, useful
CC in personalized medicine. (I) is used for prediction of the therapeutic
CC outcome of an individual with an established drug and for avoidance of
CC side effects/toxicity due to altered activity of CYP2D6 mediated by
CC different CYP2D6 alleles. (I) is useful as forensic markers. This
CC sequence corresponds to the human CYP2D6 gene.
XX
SQ Sequence 9609 BP; 2010 A; 2696 C; 3025 G; 1878 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 14; Length 9609;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CTCAGCCTCGTCACCTCACCACAG 26
||||||||||||||||||||||||
Db 6610 CTCAGCCTCGTCACCTCACCACAG 6633

RESULT 13
AEF35808
ID AEF35808 standard; DNA; 18000 BP.
XX
AC AEF35808;
XX
DT 23-MAR-2006 (first entry)
XX
DE Human cytochrome P450 2D6 DNA neighboring loci.
XX
KW diagnosis; prophylaxis; hepatitis B infection; hepatitis C infection;
KW hepatitis D infection; drug-induced hepatotoxicity; liver tumor;
KW liver cirrhosis; fibrosis; autoimmune hepatitis;
KW primary biliary cirrhosis; primary sclerosing cholangitis;
KW hemochromatosis; Wilson's disease; alpha-1 antitrypsin deficiency;
KW celiac disease; amyloidosis; gastrointestinal disease;
KW metabolic disorder; inflammation; cardiant; antiinflammatory;
KW hepatotropic; virucide; gastrointestinal-gen.; cns-gen.; metabolic;
KW immunosuppressive; cytostatic; cytochrome P450 2D6; CYP2D6; ds.
XX
OS Homo sapiens.
XX
PN WO2006003654-A2.
XX
PD 12-JAN-2006.
XX
PF 30-JUN-2005; 2005WO-IL000700.
XX
PR 01-JUL-2004; 2004US-0584179P.
XX
PA (MEDI-) MEDICAL RES FUND TEL AVIV SOURASKY MED.
XX
PI Oren R;
XX
DR WPI; 2006-090428/09.
XX
PT Determining if an individual is predisposed to fast progression of liver
PT fibrosis comprises determining a presence or absence of at least one fast
PT progression liver fibrosis-associated genotype.
XX
PS Claim 7; SEQ ID NO 10; 105pp; English.
XX
CC The invention relates to a method of determining if an individual is
CC predisposed to fast progression of liver fibrosis or liver cirrhosis
CC comprising determining a presence or absence, in a homozygous or
CC heterozygous form, of at least one fast progression liver fibrosis-
CC associated genotype in the CYP2D6, CYP3A5, CYP2E1, or APO E locus or in
CC neighboring loci of the individual, where the neighboring loci is in
CC linkage disequilibrium with the locus, thus determining if the individual
CC is predisposed to fast progression of liver fibrosis; a kit to carry out
CC the method; a method of preventing fast progression of liver fibrosis in
CC an individual, by upregulating CYP2D6 expression and/or activity; and a
CC method of determining if a drug molecule is capable of inducing or
CC accelerating development of fast progression of liver fibrosis in an
CC individual. The individual is suffering from a hepatitis viral infection
CC caused by hepatitis B, C or D virus, a hepatotoxicity (alcohol- or drug-
CC induced), a liver cancer, a non-alcoholic fatty liver disease (NAFLD), an
CC autoimmune disease (autoimmune hepatitis (AIH), primary biliary cirrhosis
CC (PBC), or primary sclerosing cholangitis (PSC)), a metabolic liver
CC disease (Hemochromatosis, Wilson's disease, or alpha 1 anti trypsin), or
CC a disease with secondary involvement of the liver (celiac disease and/or
CC amyloidosis). The method and kit are useful for determining if an
CC individual is predisposed to fast progression of liver fibrosis. The
CC method and drug are useful for preventing liver cirrhosis and fast
CC progression of liver fibrosis. This sequence is human cytochrome P450 2D6
CC DNA neighboring loci.
XX
SQ Sequence 18000 BP; 4213 A; 4884 C; 5192 G; 3711 T; 0 U; 0 Other;

Query Match 92.3%; Score 24; DB 15; Length 18000;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              |||||||||||||||||||||||
Db      12537 CTCAGCCTCGTCACCTCACCACAG 12560


RESULT 14
ADF83398
ID   ADF83398 standard; DNA; 2788 BP.
XX
AC   ADF83398;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CYP2D6 gene.
XX
KW   Human; antiemetic; setrone; cytochrome P450; CYP2D6; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003100091-A1.
XX
PD   04-DEC-2003.
XX
PF   22-MAY-2003; 2003WO-EP005366.
XX
PR   24-MAY-2002; 2002EP-00011491.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Brockmoeller HJ;
XX
DR   WPI; 2004-035165/03.
XX
PT   Use of setrones for preparing a pharmaceutical composition for treating
PT   or preventing setrone-treatable diseases in a subject having in its
PT   genome less than three copies of a polynucleotide encoding a functional
PT   CYP2D6 polypeptide.
XX
PS   Disclosure; SEQ ID NO 48; 153pp; English.
XX
CC   The present sequence comprises the human cytochrome P450 CYP2D6 gene. The
CC   invention relates to the use of setrones (antiemetics) for treating
CC   and/or preventing setrone-treatable diseases in a subject having in its
CC   genome fewer than 3 copies of a polynucleotide encoding a functional
CC   CYP2D6 polypeptide. The presence of 3 or more copies of a polynucleotide
CC   encoding a functional CYP2D6 polypeptide can be determined by determining
CC   the presence of the present sequence in the genome of the subject.
CC   Consequently, a subject having in its genome fewer than 3 copies of a
CC   polynucleotide encoding a functional CYP2D6 polypeptide is lacking the
CC   present sequence in its genome. The treatment regimen can be modified
CC   according to the genotype of the subject's CYP2D6 and/or HTR3B gene. Non-
CC   responders to antiemetic therapy can be identified on a pharmacogenetic
CC   basis, allowing a suitable therapy to be selected. The setrone-treatable
CC   diseases are postoperative nausea and/or vomiting, or nausea and/or
CC   vomiting secondary to cancer chemotherapy, radiation therapy, migraine,
CC   acetaminophen poisoning, prostacyclin therapy, and opioid treatment,
CC   spinal or epidural opioid-related pruritus, acute levodopa-induced
CC   psychosis, bulimia nervosa, fibromyalgia, chronic fatigue syndrome,
CC   obsessive-compulsive disorders, schizophrenia, alcoholism, cocaine
CC   addiction, opioid withdrawal syndrome, drug withdrawal phenomena, anxiety
CC   disorders, cognitive disturbances, neuroleptic-induced tardive
CC   dyskinesia, Tourette's syndrome, migraine headache or gastrointestinal
CC   motility disorder (all claimed).
XX
SQ   Sequence 2788 BP; 550 A; 835 C; 823 G; 580 T; 0 U; 0 Other;

  Query Match             84.6%;  Score 22;  DB 12;  Length 2788;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGCCTCGTCACCTCACCACAG 26
              |||||||||||||||||||||
Db          1 CAGCCTCGTCACCTCACCACAG 22


RESULT 15
ACN44374/c
ID   ACN44374 standard; DNA; 181684 BP.
XX
AC   ACN44374;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human genomic sequence hCG16651.
XX
KW   Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003073826-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006235.
XX
PR   01-MAR-2002; 2002US-00087192.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-328604/31.
XX
PT   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT   comprises a nucleotide sequence.
XX
PS   Claim 1; SEQ ID NO 790; 0pp; English.
XX
CC   The present invention relates to novel DNA and protein sequences which
CC   are associated with carcinomas. The sequences are useful for: (i) for
CC   screening drug candidates; (ii) for screening of bioactive agent capable
CC   of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC   a bioactive agent capable of modulating the activity of CAP; (iv) for
CC   evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC   carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC   carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC   (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC   determining Carcinoma Associated (CA) gene copy number. In addition, the
CC   CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC   carcinoma including lymphoma. The present sequence is one such CA coding
CC   sequence. Note: This patent is an equivalent to basic patent
CC   US2002182586A1, for which no sequence data was published
XX
SQ   Sequence 181684 BP; 55185 A; 34753 C; 35001 G; 55847 T; 0 U; 898 Other;

  Query Match             77.7%;  Score 20.2;  DB 11;  Length 181684;
  Best Local Similarity   88.0%;  Pred. No. 1.4e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACA 25
              ||| |||||| ||||||| ||||||
Db      12819 GACCCAGCCTGGTCACCTTACCACA 12795


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GenCore version 5.1.9

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	26	100.0	26	8	US-10-615-497-11	Sequence 11, Appl
c	2	24	92.3	3217	6	US-10-027-632-113609	Sequence 113609,
c	3	24	92.3	3217	7	US-10-027-632-113609	Sequence 113609,
	4	24	92.3	9432	3	US-09-942-310-1	Sequence 1, Appli
	5	24	92.3	9432	6	US-10-209-737-1	Sequence 1, Appli
	6	24	92.3	9432	8	US-10-712-363-1	Sequence 1, Appli
	7	24	92.3	9433	6	US-10-209-737-2	Sequence 2, Appli
	8	24	92.3	9609	9	US-10-635-780-4	Sequence 4, Appli
c	9	20.2	77.7	181684	6	US-10-087-192-790	Sequence 790, App
c	10	19	73.1	19	7	US-10-411-954-239	Sequence 239, App
c	11	19	73.1	19	8	US-10-617-070-239	Sequence 239, App
c	12	19	73.1	19	8	US-10-617-070-362	Sequence 362, App
c	13	19	73.1	19	10	US-10-956-507-239	Sequence 239, App
c	14	19	73.1	19	10	US-10-956-507-362	Sequence 362, App
	15	19	73.1	21	8	US-10-615-497-5	Sequence 5, Appli
c	16	19	73.1	23	7	US-10-411-954-269	Sequence 269, App
c	17	19	73.1	23	7	US-10-411-954-340	Sequence 340, App
c	18	19	73.1	23	8	US-10-321-039-738	Sequence 738, App
c	19	19	73.1	23	8	US-10-617-070-269	Sequence 269, App
c	20	19	73.1	23	8	US-10-617-070-340	Sequence 340, App
c	21	19	73.1	23	10	US-10-956-507-269	Sequence 269, App
c	22	19	73.1	23	10	US-10-956-507-340	Sequence 340, App
	23	18.6	71.5	828	7	US-10-225-066A-1047	Sequence 1047, Ap
	24	18.6	71.5	828	8	US-10-374-780A-2769	Sequence 2769, Ap
	25	18.6	71.5	828	10	US-10-225-066A-1047	Sequence 1047, Ap
	26	18.6	71.5	1365	8	US-10-425-114-12963	Sequence 12963, A
	27	18.6	71.5	1424	16	US-11-096-568A-31504	Sequence 31504, A
	28	18.6	71.5	1979	9	US-10-425-115-144244	Sequence 144244,
	29	18.6	71.5	3596	8	US-10-115-635-35	Sequence 35, Appl
	30	18.6	71.5	54303	9	US-10-417-375-79	Sequence 79, Appl
	31	18.6	71.5	65793	10	US-10-703-817-3	Sequence 3, Appli
	32	18.6	71.5	68200	10	US-10-840-590-3	Sequence 3, Appli
	33	18.2	70.0	1288	4	US-09-925-065A-3891	Sequence 3891, Ap
	34	18.2	70.0	1288	5	US-09-925-065A-3891	Sequence 3891, Ap
	35	18.2	70.0	1288	12	US-10-301-480-105128	Sequence 105128,
	36	18.2	70.0	1288	12	US-10-301-480-718537	Sequence 718537,
c	37	18.2	70.0	22118	3	US-09-799-462A-16	Sequence 16, Appl
c	38	18.2	70.0	22118	3	US-09-815-981-5	Sequence 5, Appli
c	39	18.2	70.0	22118	3	US-09-836-911A-16	Sequence 16, Appl
c	40	18.2	70.0	22118	3	US-09-815-979-5	Sequence 5, Appli
c	41	18.2	70.0	22118	6	US-10-125-767-16	Sequence 16, Appl
c	42	18.2	70.0	22118	6	US-10-151-081-16	Sequence 16, Appl
c	43	18.2	70.0	22118	6	US-10-287-313-16	Sequence 16, Appl
c	44	18.2	70.0	22118	6	US-10-219-694-16	Sequence 16, Appl
c	45	18.2	70.0	22118	6	US-10-235-119-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-615-497-11
; Sequence 11, Application US/10615497
; Publication No. US20040091909A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: HIGH THROUGHPUT CYTOCHROME P450 GENOTYPING
; FILE REFERENCE: 034827-1303
; CURRENT APPLICATION NUMBER: US/10/615,497
; CURRENT FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-615-497-11

Query Match 100.0%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCAGCCTCGTCACCTCACCACAG 26
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Db 1 GACTCAGCCTCGTCACCTCACCACAG 26

RESULT 2
US-10-027-632-113609/c
; Sequence 113609, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

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;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113609
;   LENGTH: 3217
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-113609

  Query Match             92.3%;  Score 24;  DB 6;  Length 3217;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
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Db       1464 CTCAGCCTCGTCACCTCACCACAG 1441


RESULT 3
US-10-027-632-113609/c
; Sequence 113609, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113609
;   LENGTH: 3217
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-113609

  Query Match             92.3%;  Score 24;  DB 7;  Length 3217;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       1464 CTCAGCCTCGTCACCTCACCACAG 1441


RESULT 4
US-09-942-310-1
; Sequence 1, Application US/09942310
; Publication No. US20030044797A1
; GENERAL INFORMATION:
;  APPLICANT: Risinger, Carl
;  APPLICANT:  Andersson, Maria K.
;  APPLICANT:  Lewander, Tommy
;  APPLICANT:  Olaisson, Erik
;  TITLE OF INVENTION: Detection of CYP2D6 Polymorphisms
;  FILE REFERENCE: GG119.1US
;  CURRENT APPLICATION NUMBER: US/09/942,310
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: GB 0021286.0
;  PRIOR FILING DATE: 2000-08-30
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9432
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-942-310-1

  Query Match             92.3%;  Score 24;  DB 3;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 5
US-10-209-737-1
; Sequence 1, Application US/10209737
; Publication No. US20030083485A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Milos, Patrice M.
;  APPLICANT:  Webb, Suzin M.
;  TITLE OF INVENTION: No. US20030083485A1el Varients Of The Human CYP2D6 Gene
;  FILE REFERENCE: PC11033AGPR
;  CURRENT APPLICATION NUMBER: US/10/209,737
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: US 60/309,111
;  PRIOR FILING DATE: 2001-07-31
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9432
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-209-737-1

  Query Match             92.3%;  Score 24;  DB 6;  Length 9432;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              ||||||||||||||||||||||||
Db       6433 CTCAGCCTCGTCACCTCACCACAG 6456


RESULT 6
US-10-712-363-1
; Sequence 1, Application US/10712363
; Publication No. US20040072235A1
; GENERAL INFORMATION:
;  APPLICANT: Dawson, Elliot P.
;  TITLE OF INVENTION: CYTOCHROME P450 GENETIC VARIATIONS
;  FILE REFERENCE: 13744-2
;  CURRENT APPLICATION NUMBER: US/10/712,363
;  CURRENT FILING DATE:  2003-11-12
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; PRIOR APPLICATION NUMBER: US 60/306,675
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 10/360,790
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/21468
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-712-363-1

Query Match 92.3%; Score 24; DB 8; Length 9432;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CTCAGCCTCGTCACCTCACCACAG 26
||||||||||||||||||||||||
Db 6433 CTCAGCCTCGTCACCTCACCACAG 6456

RESULT 7
US-10-209-737-2
; Sequence 2, Application US/10209737
; Publication No. US20030083485A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Milos, Patrice M.
; APPLICANT: Webb, Suzin M.
; TITLE OF INVENTION: No. US20030083485A1el Varients Of The Human CYP2D6 Gene
; FILE REFERENCE: PC11033AGPR
; CURRENT APPLICATION NUMBER: US/10/209,737
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/309,111
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9433
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-209-737-2

Query Match 92.3%; Score 24; DB 6; Length 9433;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CTCAGCCTCGTCACCTCACCACAG 26
||||||||||||||||||||||||
Db 6434 CTCAGCCTCGTCACCTCACCACAG 6457

RESULT 8
US-10-635-780-4
; Sequence 4, Application US/10635780
; Publication No. US20050032070A1
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie AG
; TITLE OF INVENTION: Polymorphisms in the human gene for CYP2D6 and their use in
; TITLE OF INVENTION: diagnostic and therapeutic applications
; FILE REFERENCE: VOS-43
; CURRENT APPLICATION NUMBER: US/10/635,780
; CURRENT FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 9609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-635-780-4

Query Match 92.3%; Score 24; DB 9; Length 9609;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CTCAGCCTCGTCACCTCACCACAG 26
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Db 6610 CTCAGCCTCGTCACCTCACCACAG 6633

RESULT 9
US-10-087-192-790/c
; Sequence 790, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 790
; LENGTH: 181684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(181684)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-790

Query Match 77.7%; Score 20.2; DB 6; Length 181684;
Best Local Similarity 88.0%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCAGCCTCGTCACCTCACCACA 25
||| ||||||| ||||||| |||||||
Db 12819 GACCCAGCCTGGTCACCTTACCACA 12795

RESULT 10
US-10-411-954-239/c
; Sequence 239, Application US/10411954
; Publication No. US20030235848A1
; GENERAL INFORMATION:
; APPLICANT: Neville, Matt
; APPLICANT: de Arruda Indig, Monika
; TITLE OF INVENTION: Characterization of CYP2D6 Alleles
; FILE REFERENCE: FORS-07897
; CURRENT APPLICATION NUMBER: US/10/411,954
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,819
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 356
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-411-954-239

Query Match 73.1%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          8 CCTCGTCACCTCACCACAG 26
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Db         19 CCTCGTCACCTCACCACAG 1


RESULT 11
US-10-617-070-239/c
; Sequence 239, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/617,070
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-617-070-239

  Query Match             73.1%;  Score 19;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCTCGTCACCTCACCACAG 26
              ||||||||||||||||||
Db         19 CCTCGTCACCTCACCACAG 1


RESULT 12
US-10-617-070-362/c
; Sequence 362, Application US/10617070
; Publication No. US20040096874A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/617,070
;  CURRENT FILING DATE:  2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 362
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-617-070-362

  Query Match             73.1%;  Score 19;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCTCGTCACCTCACCACAG 26
              ||||||||||||||||||
Db         19 CCTCGTCACCTCACCACAG 1


RESULT 13
US-10-956-507-239/c
; Sequence 239, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/956,507
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: US/10/617,070
;  PRIOR FILING DATE: 2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-956-507-239

  Query Match             73.1%;  Score 19;  DB 10;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCTCGTCACCTCACCACAG 26
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Db         19 CCTCGTCACCTCACCACAG 1


RESULT 14
US-10-956-507-362/c
; Sequence 362, Application US/10956507
; Publication No. US20050196771A1
; GENERAL INFORMATION:
;  APPLICANT: Neville, Matt
;  APPLICANT:  de Arruda Indig, Monika
;  APPLICANT:  Cao, Feng
;  APPLICANT:  Oldenburg, Mary C.
;  APPLICANT:  Koelbl, Jim C.
;  APPLICANT:  Aizenstein, Brian D.
;  APPLICANT:  Davey, Keith
;  TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
;  FILE REFERENCE: FORS-08195
;  CURRENT APPLICATION NUMBER: US/10/956,507
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: US/10/617,070
;  PRIOR FILING DATE: 2003-07-10
;  PRIOR APPLICATION NUMBER: 10/411,954
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,819
;  PRIOR FILING DATE: 2002-04-11
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;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 362
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-956-507-362

  Query Match             73.1%;  Score 19;  DB 10;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCTCGTCACCTCACCACAG 26
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Db         19 CCTCGTCACCTCACCACAG 1


RESULT 15
US-10-615-497-5
; Sequence 5, Application US/10615497
; Publication No. US20040091909A1
; GENERAL INFORMATION:
;  APPLICANT: HUANG, DOUG HUI
;  TITLE OF INVENTION: HIGH THROUGHPUT CYTOCHROME P450 GENOTYPING
;  FILE REFERENCE: 034827-1303
;  CURRENT APPLICATION NUMBER: US/10/615,497
;  CURRENT FILING DATE:  2003-07-07
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-615-497-5

  Query Match             73.1%;  Score 19;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCAC 21
              ||||||||||||||||||
Db          3 CTCAGCCTCGTCACCTCAC 21


Search completed: June 30, 2006, 23:53:02
Job time : 627.625 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 23:13:26 ; Search time 46.15 Seconds
(without alignments)
666.195 Million cell updates/sec

Title: US-10-615-497-11
Perfect score: 26
Sequence: 1 gactcagcctcgtcacctcaccacag 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19.6	75.4	595	7	US-11-266-748A-392199	Sequence 392199,
c	2	19.6	75.4	595	7	US-11-266-748A-482917	Sequence 482917,
c	3	19.4	74.6	620	7	US-11-266-748A-14501	Sequence 14501, A
c	4	19.2	73.8	462	7	US-11-266-748A-91028	Sequence 91028, A
	5	19.2	73.8	462	7	US-11-266-748A-143839	Sequence 143839,
c	6	18.6	71.5	355	7	US-11-266-748A-207397	Sequence 207397,
	7	18.6	71.5	355	7	US-11-266-748A-233086	Sequence 233086,
	8	18.6	71.5	387	7	US-11-266-748A-36106	Sequence 36106, A
	9	18.6	71.5	452	7	US-11-266-748A-214032	Sequence 214032,
c	10	18.6	71.5	452	7	US-11-266-748A-236799	Sequence 236799,
	11	18.6	71.5	1424	6	US-10-953-349-8689	Sequence 8689, Ap
c	12	18.2	70.0	1000	7	US-11-266-748A-201616	Sequence 201616,
c	13	18.2	70.0	22118	7	US-11-284-877-16	Sequence 16, Appl
	14	18	69.2	408	7	US-11-266-748A-422144	Sequence 422144,
	15	18	69.2	542	7	US-11-266-748A-249896	Sequence 249896,
c	16	18	69.2	542	7	US-11-266-748A-310413	Sequence 310413,
c	17	18	69.2	611	7	US-11-266-748A-41504	Sequence 41504, A
c	18	18	69.2	675	7	US-11-266-748A-2782	Sequence 2782, Ap
c	19	18	69.2	914	7	US-11-266-748A-50997	Sequence 50997, A
c	20	18	69.2	942	7	US-11-266-748A-78493	Sequence 78493, A
c	21	18	69.2	942	7	US-11-266-748A-110258	Sequence 110258,
	22	18	69.2	942	7	US-11-266-748A-131304	Sequence 131304,
c	23	18	69.2	1000	7	US-11-266-748A-202082	Sequence 202082,
c	24	18	69.2	1000	7	US-11-266-748A-288115	Sequence 288115,
	25	18	69.2	1000	7	US-11-266-748A-339544	Sequence 339544,
c	26	18	69.2	1000	7	US-11-266-748A-398928	Sequence 398928,
	27	18	69.2	1000	7	US-11-266-748A-469974	Sequence 469974,
c	28	18	69.2	1052	7	US-11-266-748A-227697	Sequence 227697,
c	29	18	69.2	1370	7	US-11-266-748A-355056	Sequence 355056,
c	30	18	69.2	1370	7	US-11-266-748A-385104	Sequence 385104,
	31	18	69.2	1370	7	US-11-266-748A-438435	Sequence 438435,
c	32	18	69.2	1451	7	US-11-266-748A-78492	Sequence 78492, A
c	33	18	69.2	1451	7	US-11-266-748A-110257	Sequence 110257,
	34	18	69.2	1451	7	US-11-266-748A-131303	Sequence 131303,
c	35	18	69.2	1734	6	US-10-953-349-32169	Sequence 32169, A
	36	18	69.2	13747	7	US-11-266-748A-28819	Sequence 28819, A
	37	18	69.2	13747	7	US-11-266-748A-62076	Sequence 62076, A
	38	18	69.2	684973	7	US-11-266-748A-32013	Sequence 32013, A
	39	17.8	68.5	809	7	US-11-266-748A-228985	Sequence 228985,
	40	17.8	68.5	882	7	US-11-266-748A-40314	Sequence 40314, A
	41	17.6	67.7	1389	7	US-11-216-545-5971	Sequence 5971, Ap
c	42	17.6	67.7	1478	6	US-10-449-902-4954	Sequence 4954, Ap
	43	17.6	67.7	2088	6	US-10-449-902-18913	Sequence 18913, A
	44	17.4	66.9	1430	6	US-10-953-349-27679	Sequence 27679, A
	45	17.4	66.9	1489	7	US-11-266-748A-180417	Sequence 180417,

ALIGNMENTS

RESULT 1
US-11-266-748A-392199
; Sequence 392199, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 392199
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-392199

Query Match 75.4%; Score 19.6; DB 7; Length 595;
Best Local Similarity 84.6%; Pred. No. 19;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
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Db        266 GACCCAGCCTCGCCTCCTCCCCACAG 291
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RESULT 2
US-11-266-748A-482917/c

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; Sequence 482917, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 482917
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-482917

  Query Match             75.4%;  Score 19.6;  DB 7;  Length 595;
  Best Local Similarity   84.6%;  Pred. No. 19;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db        330 GACCCAGCCTCGCCTCCTCCCCACAG 305


RESULT 3
US-11-266-748A-14501/c
; Sequence 14501, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14501
;   LENGTH: 620
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-14501

  Query Match             74.6%;  Score 19.4;  DB 7;  Length 620;
  Best Local Similarity   95.2%;  Pred. No. 23;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCAC 21
              |||||||||| |||||||||
Db        140 GACTCAGCCTCTTCACCTCAC 120


RESULT 4
US-11-266-748A-91028/c
; Sequence 91028, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91028
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-91028

  Query Match             73.8%;  Score 19.2;  DB 7;  Length 462;
  Best Local Similarity   87.5%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              | ||||||||||||||| |||||
Db         86 GCCTCAGCCTCGTCACCCAACCAC 63


RESULT 5
US-11-266-748A-143839
; Sequence 143839, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
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;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 143839
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-143839

  Query Match             73.8%;  Score 19.2;  DB 7;  Length 462;
  Best Local Similarity   87.5%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              | ||||||||||||||||  |||||
Db        377 GCCTCAGCCTCGTCACCCAACCAC 400


RESULT 6
US-11-266-748A-207397/c
; Sequence 207397, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 207397
;   LENGTH: 355
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (235)..(235)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-207397

  Query Match             71.5%;  Score 18.6;  DB 7;  Length 355;
  Best Local Similarity   84.0%;  Pred. No. 48;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
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Db        125 ACTCAGCCCCATGACCTGACCACAG 101


RESULT 7
US-11-266-748A-233086
; Sequence 233086, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 233086
;   LENGTH: 355
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (121)..(121)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-233086

  Query Match             71.5%;  Score 18.6;  DB 7;  Length 355;
  Best Local Similarity   84.0%;  Pred. No. 48;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
              |||||||| | | |||| |||||||
Db        231 ACTCAGCCCCATGACCTGACCACAG 255


RESULT 8
US-11-266-748A-36106
; Sequence 36106, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
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;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36106
;   LENGTH: 387
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-36106

  Query Match             71.5%;  Score 18.6;  DB 7;  Length 387;
  Best Local Similarity   84.0%;  Pred. No. 49;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
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Db        190 ACTCACCCTGGTATCCTCACCACAG 214


RESULT 9
US-11-266-748A-214032
; Sequence 214032, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 214032
;   LENGTH: 452
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-214032

  Query Match             71.5%;  Score 18.6;  DB 7;  Length 452;
  Best Local Similarity   84.0%;  Pred. No. 50;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
              ||||| ||| ||  ||||||||||
Db        266 ACTCACCCTGGTATCCTCACCACAG 290


RESULT 10
US-11-266-748A-236799/c
; Sequence 236799, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 236799
;   LENGTH: 452
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-236799

  Query Match             71.5%;  Score 18.6;  DB 7;  Length 452;
  Best Local Similarity   84.0%;  Pred. No. 50;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
              ||||| ||| ||  ||||||||||
Db        187 ACTCACCCTGGTATCCTCACCACAG 163


RESULT 11
US-10-953-349-8689
; Sequence 8689, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8689
;   LENGTH: 1424
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-8689
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Query Match 71.5%; Score 18.6; DB 6; Length 1424;
Best Local Similarity 84.0%; Pred. No. 58;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
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Db        362 ACTCAGCCTCGTCACTTCTGCAAAG 386
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RESULT 12
US-11-266-748A-201616/c
; Sequence 201616, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 201616
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-201616

Query Match 70.0%; Score 18.2; DB 7; Length 1000;
Best Local Similarity 87.0%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 TCAGCCTCGTCACCTCACCACAG 26
              ||| ||| ||| ||||||||||||
Db        838 TCACCCTGGTCGCCTCACCACAG 816
```

RESULT 13
US-11-284-877-16/c
; Sequence 16, Application US/11284877
; Publication No. US20060095984A1
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
; FOR PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 12390 El Camino Real
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/284,877
; FILING DATE: 21-Nov-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/808,689
; FILING DATE: 24-MAR-2004
; APPLICATION NUMBER: 10/219,694
; FILING DATE: 14-AUG-2002
; APPLICATION NUMBER: 10/151,081
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/151,078
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/125,767
; FILING DATE: 17-APR-2002
; APPLICATION NUMBER: 10/287,313
; FILING DATE: 01-NOV-2002
; APPLICATION NUMBER: 09/799,462
; FILING DATE: 05-MAR-2001
; APPLICATION NUMBER: 09/724,872
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,726
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,693
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 08/835,682
; FILING DATE: 10-APR-1997
; APPLICATION NUMBER: 08/695,191
; FILING DATE: 07-AUG-1996
; APPLICATION NUMBER: 08/682,080
; FILING DATE: 15-JUL-1996
; APPLICATION NUMBER: 08/629,822
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 17084-004018/402Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-678-4777
; TELEFAX: 202-626-7796
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22118 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-284-877-16

Query Match 70.0%; Score 18.2; DB 7; Length 22118;
Best Local Similarity 87.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          4 TCAGCCTCGTCACCTCACCACAG 26
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Db       3547 TCACCCTGGTCGCCTCACCACAG 3525
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RESULT 14
US-11-266-748A-422144
; Sequence 422144, Application US/11266748A
; Publication No. US20060134663A1

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; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 422144
;   LENGTH: 408
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-422144

  Query Match             69.2%;  Score 18;  DB 7;  Length 408;
  Best Local Similarity   80.8%;  Pred. No. 90;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              |||||| ||| |||||  ||||| ||
Db        144 GACTCAACCTTGTCACAACACCAAAG 169


RESULT 15
US-11-266-748A-249896
; Sequence 249896, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 249896
;   LENGTH: 542
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-249896

  Query Match             69.2%;  Score 18;  DB 7;  Length 542;
  Best Local Similarity   80.8%;  Pred. No. 93;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              |||||  |||||  ||||||  |||||
Db        125 GACTCCGCCTCCCCACCTCTGCACAG 150


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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:17:54 ; Search time 101.725 Seconds
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Title: US-10-615-497-11
Perfect score: 26
Sequence: 1 gactcagcctcgtcacctcaccacag 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19.6	75.4	601	3	US-09-949-016-21140	Sequence 21140, A
c	2	19.6	75.4	601	3	US-09-949-016-21141	Sequence 21141, A
c	3	19.6	75.4	601	3	US-09-949-016-21142	Sequence 21142, A
c	4	19.6	75.4	601	3	US-09-949-016-47508	Sequence 47508, A
c	5	19.6	75.4	601	3	US-09-949-016-47509	Sequence 47509, A
c	6	19.6	75.4	601	3	US-09-949-016-47510	Sequence 47510, A
	7	19.6	75.4	31467	3	US-09-949-016-13134	Sequence 13134, A
	8	19.6	75.4	31868	3	US-09-949-016-11907	Sequence 11907, A
	9	19.4	74.6	74790	3	US-09-949-016-15321	Sequence 15321, A
c	10	19.2	73.8	564	3	US-09-621-976-3691	Sequence 3691, Ap
	11	19.2	73.8	8355	3	US-08-406-030A-23	Sequence 23, Appl
c	12	18.6	71.5	601	3	US-09-949-016-39184	Sequence 39184, A
c	13	18.6	71.5	601	3	US-09-949-016-39185	Sequence 39185, A
c	14	18.6	71.5	601	3	US-09-949-016-39186	Sequence 39186, A
c	15	18.6	71.5	601	3	US-09-949-016-167829	Sequence 167829,
c	16	18.6	71.5	601	3	US-09-949-016-167830	Sequence 167830,
c	17	18.6	71.5	601	3	US-09-949-016-167831	Sequence 167831,
c	18	18.6	71.5	22906	3	US-09-949-016-16471	Sequence 16471, A
c	19	18.6	71.5	28809	3	US-09-949-016-12825	Sequence 12825, A
c	20	18.2	70.0	22118	3	US-09-815-981A-5	Sequence 5, Appli
	21	18.2	70.0	29720	3	US-09-949-016-16521	Sequence 16521, A
c	22	18	69.2	283	3	US-09-513-999C-34788	Sequence 34788, A
	23	18	69.2	601	3	US-09-949-016-202376	Sequence 202376,
	24	18	69.2	601	3	US-09-949-016-202377	Sequence 202377,
c	25	18	69.2	1535	3	US-09-620-312D-288	Sequence 288, App
c	26	18	69.2	3914	3	US-10-104-047-850	Sequence 850, App
	27	18	69.2	11613	2	US-08-484-044-10	Sequence 10, Appl
c	28	18	69.2	84571	3	US-09-949-016-17420	Sequence 17420, A
	29	18	69.2	325791	3	US-09-768-185A-1	Sequence 1, Appli
	30	17.8	68.5	601	3	US-09-949-016-154710	Sequence 154710,
c	31	17.8	68.5	275110	3	US-09-949-016-12706	Sequence 12706, A
c	32	17.8	68.5	275110	3	US-09-949-016-16070	Sequence 16070, A
	33	17.6	67.7	460	3	US-09-401-064-169	Sequence 169, App
	34	17.6	67.7	601	3	US-09-949-016-33152	Sequence 33152, A
	35	17.6	67.7	601	3	US-09-949-016-59055	Sequence 59055, A
	36	17.6	67.7	601	3	US-09-949-016-65664	Sequence 65664, A
c	37	17.6	67.7	601	3	US-09-949-016-126754	Sequence 126754,
c	38	17.6	67.7	601	3	US-09-949-016-126803	Sequence 126803,
c	39	17.6	67.7	601	3	US-09-949-016-126852	Sequence 126852,
c	40	17.6	67.7	601	3	US-09-949-016-134387	Sequence 134387,
c	41	17.6	67.7	601	3	US-09-949-016-134436	Sequence 134436,
c	42	17.6	67.7	601	3	US-09-949-016-134485	Sequence 134485,
	43	17.6	67.7	601	3	US-09-949-002-7214	Sequence 7214, Ap
	44	17.6	67.7	2581	3	US-10-104-047-1373	Sequence 1373, Ap
	45	17.6	67.7	6817	3	US-09-949-016-13665	Sequence 13665, A

ALIGNMENTS

RESULT 1
US-09-949-016-21140/c
; Sequence 21140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21140
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21140

Query Match 75.4%; Score 19.6; DB 3; Length 601;
Best Local Similarity 84.6%; Pred. No. 38;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db        102 GACCCAGCCTCGCCTCCTCCCCACAG 77
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RESULT 2
US-09-949-016-21141/c
; Sequence 21141, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21141
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-21141

  Query Match             75.4%;  Score 19.6;  DB 3;  Length 601;
  Best Local Similarity   84.6%;  Pred. No. 38;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db        152 GACCCAGCCTCGCCTCCTCCCCACAG 127


RESULT 3
US-09-949-016-21142/c
; Sequence 21142, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21142
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-21142

  Query Match             75.4%;  Score 19.6;  DB 3;  Length 601;
  Best Local Similarity   84.6%;  Pred. No. 38;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db        341 GACCCAGCCTCGCCTCCTCCCCACAG 316


RESULT 4
US-09-949-016-47508/c
; Sequence 47508, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47508
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-47508

  Query Match             75.4%;  Score 19.6;  DB 3;  Length 601;
  Best Local Similarity   84.6%;  Pred. No. 38;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db        102 GACCCAGCCTCGCCTCCTCCCCACAG 77


RESULT 5
US-09-949-016-47509/c
; Sequence 47509, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47509
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-47509

  Query Match             75.4%;  Score 19.6;  DB 3;  Length 601;
  Best Local Similarity   84.6%;  Pred. No. 38;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db        152 GACCCAGCCTCGCCTCCTCCCCACAG 127


RESULT 6
US-09-949-016-47510/c
; Sequence 47510, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47510
;   LENGTH: 601
;   TYPE: DNA
```

```
;   ORGANISM: Human
US-09-949-016-47510

  Query Match             75.4%;  Score 19.6;  DB 3;  Length 601;
  Best Local Similarity   84.6%;  Pred. No. 38;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db        341 GACCCAGCCTCGCCTCCTCCCCACAG 316


RESULT 7
US-09-949-016-13134
; Sequence 13134, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13134
;   LENGTH: 31467
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(31467)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13134

  Query Match             75.4%;  Score 19.6;  DB 3;  Length 31467;
  Best Local Similarity   84.6%;  Pred. No. 48;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db      22561 GACCCAGCCTCGCCTCCTCCCCACAG 22586


RESULT 8
US-09-949-016-11907
; Sequence 11907, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11907
;   LENGTH: 31868
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(31868)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11907

  Query Match             75.4%;  Score 19.6;  DB 3;  Length 31868;
  Best Local Similarity   84.6%;  Pred. No. 48;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCACAG 26
              ||| |||||||| | |||| ||||||
Db      22962 GACCCAGCCTCGCCTCCTCCCCACAG 22987


RESULT 9
US-09-949-016-15321
; Sequence 15321, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15321
;   LENGTH: 74790
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15321

  Query Match             74.6%;  Score 19.4;  DB 3;  Length 74790;
  Best Local Similarity   95.2%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCAC 21
              |||||||||||| |||||||||
Db      24327 GACTCAGCCTCTTCACCTCAC 24347


RESULT 10
US-09-621-976-3691/c
; Sequence 3691, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 3691
;   LENGTH: 564
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 301..483
US-09-621-976-3691

  Query Match             73.8%;  Score 19.2;  DB 3;  Length 564;
```

```
  Best Local Similarity   87.5%;  Pred. No. 55;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACTCAGCCTCGTCACCTCACCAC 24
              | ||||||||||||||||  |||||
Db        153 GCCTCAGCCTCGTCACCCAACCAC 130


RESULT 11
US-08-406-030A-23
; Sequence 23, Application US/08406030A
; Patent No. 6270989
;  GENERAL INFORMATION:
;    APPLICANT:  Treco, Douglas A.
;    APPLICANT:  Heartlein, Michael W.
;    APPLICANT:  Hauge, Brian M.
;    APPLICANT:  Selden, Richard F
;    TITLE OF INVENTION:  Protein Production and Delivery
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.c.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/406,030A
;      FILING DATE:  17-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/243,391
;      FILING DATE:  13-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/985,586
;      FILING DATE:  03-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/911,533
;      FILING DATE:  10-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,840
;      FILING DATE:  05-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/789,188
;      FILING DATE:  05-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/11704
;      FILING DATE:  02-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/09627
;      FILING DATE:  05-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  TKT95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8355 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-406-030A-23

  Query Match             73.8%;  Score 19.2;  DB 3;  Length 8355;
```

```
  Best Local Similarity   87.5%;  Pred. No. 65;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CTCAGCCTCGTCACCTCACCACAG 26
              |||| || | ||||||||||||||
Db       5532 CTCAACCACATCACCTCACCACAG 5555


RESULT 12
US-09-949-016-39184/c
; Sequence 39184, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39184
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-39184

  Query Match             71.5%;  Score 18.6;  DB 3;  Length 601;
  Best Local Similarity   84.0%;  Pred. No. 99;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
              ||||| ||| ||  ||||||||||
Db        567 ACTCACCCTGGTATCCTCACCACAG 543


RESULT 13
US-09-949-016-39185/c
; Sequence 39185, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39185
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-39185

  Query Match             71.5%;  Score 18.6;  DB 3;  Length 601;
  Best Local Similarity   84.0%;  Pred. No. 99;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
              ||||| ||| ||  ||||||||||
```

```
Db         47 ACTCACCCTGGTATCCTCACCACAG 23


RESULT 14
US-09-949-016-39186/c
; Sequence 39186, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39186
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-39186

  Query Match             71.5%;  Score 18.6;  DB 3;  Length 601;
  Best Local Similarity   84.0%;  Pred. No. 99;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
              ||||| ||| ||  ||||||||||
Db         33 ACTCACCCTGGTATCCTCACCACAG 9


RESULT 15
US-09-949-016-167829/c
; Sequence 167829, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167829
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-167829

  Query Match             71.5%;  Score 18.6;  DB 3;  Length 601;
  Best Local Similarity   84.0%;  Pred. No. 99;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACTCAGCCTCGTCACCTCACCACAG 26
              ||||| ||| ||  ||||||||||
Db        567 ACTCACCCTGGTATCCTCACCACAG 543


Search completed: July  1, 2006, 01:23:12
Job time : 102.725 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:12:31 ; Search time 1362.53 Seconds
(without alignments)
1736.522 Million cell updates/sec

Title: US-10-615-497-14
Perfect score: 37
Sequence: 1 ctgactgactgactctcttgttgaccaggctggagtg 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30.6	82.7	145344	12	AC027127	AC027127 Homo sapi
c	2	30.6	82.7	161192	5	AC022014	AC022014 Homo sapi
	3	30.6	82.7	165228	5	AC005325	AC005325 Homo sapi
	4	30.6	82.7	165821	12	AC022005	AC022005 Homo sapi
	5	30.6	82.7	176010	12	AC069125	AC069125 Homo sapi
	6	30.6	82.7	178274	12	AC022006	AC022006 Homo sapi
	7	30.6	82.7	180508	5	AC026168	AC026168 Homo sapi
c	8	30.6	82.7	180736	12	AP003030	AP003030 Homo sapi
c	9	30.6	82.7	189310	5	AP006215	AP006215 Homo sapi
c	10	30.6	82.7	191957	5	AC015845	AC015845 Homo sapi
	11	30.6	82.7	196373	12	AC022004	AC022004 Homo sapi
	12	30.6	82.7	225231	12	AC024733	AC024733 Homo sapi
c	13	29.6	80.0	857	7	BV520177	BV520177 G591P6634
c	14	29.6	80.0	183155	5	BS000175	BS000175 Pan trogl
	15	29.6	80.0	187607	5	AC010329	AC010329 Homo sapi
	16	29	78.4	55965	5	AC104653	AC104653 Homo sapi
c	17	29	78.4	171779	12	AC150825	AC150825 Callithri
	18	28.6	77.3	816	2	BD021440	BD021440 Novel gen
	19	28.6	77.3	816	2	BD101378	BD101378 Novel gen
	20	28.6	77.3	73433	5	AC068889	AC068889 Homo sapi
	21	28.6	77.3	74371	5	AC005369	AC005369 Homo sapi
c	22	28.6	77.3	77908	5	AC008609	AC008609 Homo sapi
	23	28.6	77.3	80630	5	AL359972	AL359972 Human DNA
	24	28.6	77.3	83412	5	AC092843	AC092843 Homo sapi
c	25	28.6	77.3	102351	12	AL138848	AL138848 Homo sapi
	26	28.6	77.3	114475	5	AC108082	AC108082 Homo sapi
c	27	28.6	77.3	148005	12	AC024944	AC024944 Homo sapi
	28	28.6	77.3	153137	5	AC016995	AC016995 Homo sapi
	29	28.6	77.3	155112	12	AC124847	AC124847 Homo sapi
c	30	28.6	77.3	155218	12	AC021879	AC021879 Homo sapi
c	31	28.6	77.3	155953	5	AC018648	AC018648 Homo sapi
	32	28.6	77.3	156169	5	AP005062	AP005062 Homo sapi
c	33	28.6	77.3	159392	12	AC148829	AC148829 Pan trogl
c	34	28.6	77.3	159644	5	AP000820	AP000820 Homo sapi
	35	28.6	77.3	159766	5	AC104942	AC104942 Homo sapi
c	36	28.6	77.3	164056	12	AC079593	AC079593 Homo sapi
c	37	28.6	77.3	164394	5	AC008706	AC008706 Homo sapi
	38	28.6	77.3	166447	12	AC022986	AC022986 Homo sapi
c	39	28.6	77.3	166697	12	AC021103	AC021103 Homo sapi
	40	28.6	77.3	167776	12	AC026192	AC026192 Homo sapi
	41	28.6	77.3	168366	5	AL353667	AL353667 Human DNA
c	42	28.6	77.3	169303	5	AL354808	AL354808 Human DNA
	43	28.6	77.3	169405	5	AC092800	AC092800 Homo sapi
c	44	28.6	77.3	169883	12	AC023407	AC023407 Homo sapi
c	45	28.6	77.3	170761	5	CNS05TER	AL359240 Human chr

ALIGNMENTS

RESULT 1
AC027127
LOCUS AC027127 145344 bp DNA linear HTG 29-MAY-2000
DEFINITION Homo sapiens chromosome 3 clone RP11-611B18 map 3p, WORKING DRAFT SEQUENCE, 33 unordered pieces.
ACCESSION AC027127
VERSION AC027127.3 GI:8101251
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 145344)
AUTHORS Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,Y., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Yu,J. and Yang,H.
TITLE Chromosome 3p genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 145344)
AUTHORS Wang,R., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J. and Yang,H.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China
COMMENT On May 29, 2000 this sequence version replaced gi:7644458.
----------Genome Center
Center:Beijing Center
Center code:Beijing

```
Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
-------------- Project Information
Center project name:1% project
Center clone name: RP11-611B18
-------------- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 130327 bases at least Q40
Consensus quality: 140019 bases at least Q30
Consensus quality: 146327 bases at least Q20
Insert size: 124982; sum-of-contigs
Quality coverage:   3.00x in Q20 bases;sum-of-contigs
--------------.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*       1     1038: contig of 1038 bp in length
*    1039     1138: gap of unknown length
*    1139     2279: contig of 1141 bp in length
*    2280     2379: gap of unknown length
*    2380     3742: contig of 1363 bp in length
*    3743     3842: gap of unknown length
*    3843     5210: contig of 1368 bp in length
*    5211     5310: gap of unknown length
*    5311     6981: contig of 1671 bp in length
*    6982     7081: gap of unknown length
*    7082     9185: contig of 2104 bp in length
*    9186     9285: gap of unknown length
*    9286    11080: contig of 1795 bp in length
*   11081    11180: gap of unknown length
*   11181    12930: contig of 1750 bp in length
*   12931    13030: gap of unknown length
*   13031    14771: contig of 1741 bp in length
*   14772    14871: gap of unknown length
*   14872    17811: contig of 2940 bp in length
*   17812    17911: gap of unknown length
*   17912    21619: contig of 3708 bp in length
*   21620    21719: gap of unknown length
*   21720    25427: contig of 3708 bp in length
*   25428    25527: gap of unknown length
*   25528    27725: contig of 2198 bp in length
*   27726    27825: gap of unknown length
*   27826    31640: contig of 3815 bp in length
*   31641    31740: gap of unknown length
*   31741    36812: contig of 5072 bp in length
*   36813    36912: gap of unknown length
*   36913    40076: contig of 3164 bp in length
*   40077    40176: gap of unknown length
*   40177    44847: contig of 4671 bp in length
*   44848    44947: gap of unknown length
*   44948    49560: contig of 4613 bp in length
*   49561    49660: gap of unknown length
*   49661    53975: contig of 4315 bp in length
*   53976    54075: gap of unknown length
*   54076    59144: contig of 5069 bp in length
*   59145    59244: gap of unknown length
*   59245    64078: contig of 4834 bp in length
*   64079    64178: gap of unknown length
*   64179    69043: contig of 4865 bp in length
*   69044    69143: gap of unknown length
*   69144    74986: contig of 5843 bp in length
*   74987    75086: gap of unknown length
*   75087    80698: contig of 5612 bp in length
*   80699    80798: gap of unknown length
*   80799    85770: contig of 4972 bp in length
*   85771    85870: gap of unknown length
*   85871    91345: contig of 5475 bp in length
*   91346    91445: gap of unknown length
*   91446    97171: contig of 5726 bp in length
*   97172    97271: gap of unknown length
*   97272   105327: contig of 8056 bp in length
*  105328   105427: gap of unknown length
*  105428   113058: contig of 7631 bp in length
*  113059   113158: gap of unknown length
*  113159   118068: contig of 4910 bp in length
*  118069   118168: gap of unknown length
*  118169   125212: contig of 7044 bp in length
*  125213   125312: gap of unknown length
*  125313   135600: contig of 10288 bp in length
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                     /chromosome="3"
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                     /clone="RP11-611B18"
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     misc_feature    5311. .6981
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     gap             6982. .7081
                     /estimated_length=unknown
     misc_feature    7082. .9185
                     /note="assembly_name:Contig24"
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     misc_feature    9286. .11080
                     /note="assembly_name:Contig25"
     gap             11081. .11180
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     misc_feature    11181. .12930
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                     /note="assembly_name:Contig34"
     gap             40077. .40176

  Query Match             82.7%;  Score 30.6;  DB 12;  Length 145344;
  Best Local Similarity   89.2%;  Pred. No. 0.057;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||||||  | |||||||||| ||||||||||||
Db      86581 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 86617


RESULT 2
AC022014/c
LOCUS       AC022014               161192 bp    DNA     linear   PRI 11-OCT-2000
DEFINITION  Homo sapiens chromosome 11 clone RP11-91E22 map 11q, complete
            sequence.
ACCESSION   AC022014
VERSION     AC022014.3  GI:10765023
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 161192)
  AUTHORS   Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
            Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
            He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G.,
            Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
            Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S.,
            Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J.,
            Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D.,
            Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
            Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
            Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
  TITLE     Chromosome 11q genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 161192)
  AUTHORS   Qi,X., Hu,S., Dong,W., Zhang,X., Wang,J., Zhang,Y., Zhang,H.,
            Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
            Niu,Y., Wang,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
            Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L.,
            Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
            Feng,X., Yu,J. and Yang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
REFERENCE   3  (bases 1 to 161192)
  AUTHORS   Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
            Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
            He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G.,
            Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
            Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S.,
            Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J.,
            Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D.,
            Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
            Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
            Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-2000) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
COMMENT     On Oct 11, 2000 this sequence version replaced gi:6862635.
            -------------Genome Center
            Center:Beijing Center
            Center code:Beijing
            Website:http://hgc.igtp.ac.cn
            http://www.genomics.org.cn
            Contact:hgc@igtp.ac.cn
            -------------- Project Information
            Center project name:1% project
            Center clone name: RP11-91E22
            -------------- Summary Statistics
            Sequencing vector: pUC18; 100% of reads
            Chemistry: Dye-terminator: ET 55% of reads
            Chemistry: Dye-terminator Big Dye; 45% of reads
            Assembly program: Phrap; version 0.990329
            Consensus quality: 684 bases at least Q40
            Consensus quality: 854 bases at least Q30
            Consensus quality: 894 bases at least Q20
            Insert size: 882; sum-of-contigs
            Quality coverage:   1.83x in Q20 bases;sum-of-contigs
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FEATURES                Location/Qualifiers
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ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 5;  Length 161192;
  Best Local Similarity   89.2%;  Pred. No. 0.059;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||||||  | |||||||||| ||||||||||||
Db      54865 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 54829


RESULT 3
AC005325
LOCUS       AC005325               165228 bp    DNA     linear   PRI 31-JUL-1998
DEFINITION  Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.
ACCESSION   AC005325
VERSION     AC005325.1  GI:3366581
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 165228)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone hRPK.60_A_24
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 165228)
  AUTHORS   Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boatin,C.,
            Boutwell,C., Brown,A., Castle,A., Cerny,J., Cooke,P., Depayre,E.,
            Devon,K., Dewar,K., Donelan,L., Etemadi,S., Ferreira,P.,
            FitzHugh,W., Forrest,C., Funke,R., Gage,D., Gardyna,S.,
            Gensheimer,S., Geraigery,K., Gilmartin,T., Grant,G., Hagos,B.,
            Harris,K., Horton,L., Howland,J.C., Jacotot,L., Kann,L.,
            Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
            Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
            Nahf,R., Naylor,J., Niloff,M., O'Connor,T., Pavlin,B., Peterson,K.,
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            Stange-Thomann,N., Stilwell,J., Stojanovic,N., Stone,C.,
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            Subramanian,A., Torruella-Miller,I., Vassiliev,H., Vo,A.,
            Wagner,A., Wang,B., Wheeler,J., Wu,Y., Ye,W.J., Zhao,J. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUL-1998) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 165228)
  AUTHORS   Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boutwell,C.,
            Brown,A., Castle,A., Cerny,J., Cooke,P., Depayre,E., Devon,K.,
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            Molla,M., Morris,W., Morrow,J., Mychaleckyj,J., Nahf,R., Naylor,J.,
            Niloff,M., O'Connor,T., Pavlin,B., Peterson,K., Riley,R.,
            Roberts,D., Roy,A., Stange-Thomann,N., Stilwell,J., Stojanovic,N.,
            Stone,C., Subramanian,A., Torruella-Miller,I., Vassiliev,H., Vo,A.,
            Wagner,A., Wang,B., Wheeler,J., Wu,Y., Ye,W.J., Zhao,J. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-1998) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jul 31, 1998 this sequence version replaced gi:3355498.
            All repeats were identified using RepeatMasker: Smit, A.F.A. &
            Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html.
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     repeat_region   complement(1770. .2048)
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     repeat_region   complement(34259. .34374)
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     repeat_region   38534. .38574

  Query Match             82.7%;  Score 30.6;  DB 5;  Length 165228;
  Best Local Similarity   89.2%;  Pred. No. 0.06;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| ||| ||| |||||||||||| ||||||||||||
Db      16933 CTGTCTGTCTGCCTCTCTTGTTGCCCAGGCTGGAGTG 16969


RESULT 4
AC022005
LOCUS       AC022005              165821 bp    DNA     linear   HTG 03-FEB-2000
DEFINITION  Homo sapiens chromosome 3p clone RP11-378N17, WORKING DRAFT
            SEQUENCE, 19 unordered pieces.
ACCESSION   AC022005
VERSION     AC022005.1  GI:6742900
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 165821)
  AUTHORS   Wang,J., Hu,S., Dong,W., Zhang,X., Wang,X., Zhang,Y., Zhang,H.,
            Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
            Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
            Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L.,
            Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
            Feng,X., Yu,J. and Yang,H.
  TITLE     Chromosome 3p genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 165821)
  AUTHORS   Wang,J., Hu,S., Dong,W., Zhang,X., Wang,X., Zhang,Y., Zhang,H.,
            Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
            Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
            Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L.,
            Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
            Feng,X., Yu,J. and Yang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
COMMENT     * NOTE: This is a 'working draft' sequence. It currently
            * consists of 19 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2538: contig of 2538 bp in length
            *                   gap of unknown length
            *     2539     4630: contig of 2092 bp in length
            *                   gap of unknown length
            *     4631     6800: contig of 2170 bp in length
            *                   gap of unknown length
            *     6801     9155: contig of 2355 bp in length
            *                   gap of unknown length
            *     9156    12743: contig of 3588 bp in length
            *                   gap of unknown length
            *    12744    16226: contig of 3483 bp in length
            *                   gap of unknown length
            *    16227    21074: contig of 4848 bp in length
            *                   gap of unknown length
            *    21075    23938: contig of 2864 bp in length
            *                   gap of unknown length
            *    23939    31147: contig of 7209 bp in length
            *                   gap of unknown length
            *    31148    36521: contig of 5374 bp in length
            *                   gap of unknown length
            *    36522    44575: contig of 8054 bp in length
            *                   gap of unknown length
            *    44576    53034: contig of 8459 bp in length
            *                   gap of unknown length
            *    53035    59574: contig of 6540 bp in length
            *                   gap of unknown length
            *    59575    67242: contig of 7668 bp in length
            *                   gap of unknown length
            *    67243    82668: contig of 15426 bp in length
            *                   gap of unknown length
            *    82669    97713: contig of 15045 bp in length
            *                   gap of unknown length
            *    97714   118732: contig of 21019 bp in length
            *                   gap of unknown length
            *   118733   141508: contig of 22776 bp in length
            *                   gap of unknown length
            *   141509   165821: contig of 24313 bp in length.
FEATURES             Location/Qualifiers
     source          1. .165821
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3p"
                     /clone="RP11-378N17"
ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 12;  Length 165821;
  Best Local Similarity   89.2%;  Pred. No. 0.06;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||||||  | |||||||| ||||||||||||
Db     125291 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 125327


RESULT 5
AC069125
LOCUS       AC069125              176010 bp    DNA     linear   HTG 31-AUG-2000
DEFINITION  Homo sapiens chromosome 17 clone RP11-102J6, WORKING DRAFT
            SEQUENCE, 9 unordered pieces.
ACCESSION   AC069125
VERSION     AC069125.3  GI:9954820
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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REFERENCE   1  (bases 1 to 176010)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 176010)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAY-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Aug 31, 2000 this sequence version replaced gi:9910073.

            ----------------- Genome Center -----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0102J06
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 100% of reads
            Chemistry: Dye-terminator Big Dye; 0% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 167650 bases at least Q40
            Consensus quality: 170264 bases at least Q30
            Consensus quality: 172237 bases at least Q20
            Insert size: 182000; agarose-fp
            Insert size: 175210; sum-of-contigs
            Quality coverage: 5.02 in Q20 bases; agarose-fp
            Quality coverage: 5.24 in Q20 bases; sum-of-contigs
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 9 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     8222: contig of 8222 bp in length
            *    8223     8322: gap of unknown length
            *    8323    17997: contig of 9675 bp in length
            *   17998    18097: gap of unknown length
            *   18098    32171: contig of 14074 bp in length
            *   32172    32271: gap of unknown length
            *   32272    56087: contig of 23816 bp in length
            *   56088    56187: gap of unknown length
            *   56188   163194: contig of 107007 bp in length
            *  163195   163294: gap of unknown length
            *  163295   164386: contig of 1092 bp in length
            *  164387   164486: gap of unknown length
            *  164487   166551: contig of 2065 bp in length
            *  166552   166651: gap of unknown length
            *  166652   170059: contig of 3408 bp in length
            *  170060   170159: gap of unknown length
            *  170161   176010: contig of 5851 bp in length.
FEATURES             Location/Qualifiers
     source          1. .176010
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="17"
                     /clone="RP11-102J6"
     misc_feature    1. .8222
                     /note="assembly_name:Contig10"
     gap             8223. .8322
                     /estimated_length=unknown
     misc_feature    8323. .17997
                     /note="assembly_name:Contig11"
     gap             17998. .18097
                     /estimated_length=unknown
     misc_feature    18098. .32171
                     /note="assembly_name:Contig12"
     gap             32172. .32271
                     /estimated_length=unknown
     misc_feature    32272. .56087
                     /note="assembly_name:Contig13
                     clone_end:SP6
                     vector_side:right"
     gap             56088. .56187
                     /estimated_length=unknown
     misc_feature    56188. .163194
                     /note="assembly_name:Contig14
                     clone_end:T7
                     vector_side:right"
     gap             163195. .163294
                     /estimated_length=unknown
     misc_feature    163295. .164386
                     /note="assembly_name:Contig3"
     gap             164387. .164486
                     /estimated_length=unknown
     misc_feature    164487. .166551
                     /note="assembly_name:Contig7"
     gap             166552. .166651
                     /estimated_length=unknown
     misc_feature    166652. .170059
                     /note="assembly_name:Contig8"
     gap             170060. .170159
                     /estimated_length=unknown
     misc_feature    170160. .176010
                     /note="assembly_name:Contig9"
ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 12;  Length 176010;
  Best Local Similarity   89.2%;  Pred. No. 0.061;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| ||| ||| |||||||||||| ||||||||||||
Db     113132 CTGTCTGTCTGCCTCTCTTGTTGCCCAGGCTGGAGTG 113168


RESULT 6
AC022006
LOCUS       AC022006              178274 bp    DNA     linear   HTG 03-FEB-2000
DEFINITION  Homo sapiens chromosome 3p clone RP11-429D11, WORKING DRAFT
            SEQUENCE, 15 unordered pieces.
ACCESSION   AC022006
VERSION     AC022006.2  GI:6862652
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 178274)
  AUTHORS   Zhang,Y., Hu,S., Dong,W., Zhang,X., Wang,J., Wang,X., Zhang,H.,
            Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
            Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
            Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L.,
            Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
            Feng,X., Yu,J. and Yang,H.
  TITLE     Chromosome 3p genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 178274)
  AUTHORS   Zhang,Y., Hu,S., Dong,W., Zhang,X., Wang,J., Wang,X., Zhang,H.,
            Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
            Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
            Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L.,
            Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
            Feng,X., Yu,J. and Yang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
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COMMENT     On Feb 3, 2000 this sequence version replaced gi:6742894.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 15 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2914: contig of 2914 bp in length
            *                   gap of unknown length
            *     2915     5774: contig of 2860 bp in length
            *                   gap of unknown length
            *     5775     9976: contig of 4202 bp in length
            *                   gap of unknown length
            *     9977    13868: contig of 3892 bp in length
            *                   gap of unknown length
            *    13869    17948: contig of 4080 bp in length
            *                   gap of unknown length
            *    17949    22064: contig of 4116 bp in length
            *                   gap of unknown length
            *    22065    27119: contig of 5055 bp in length
            *                   gap of unknown length
            *    27120    38081: contig of 10962 bp in length
            *                   gap of unknown length
            *    38082    49051: contig of 10970 bp in length
            *                   gap of unknown length
            *    49052    63091: contig of 14040 bp in length
            *                   gap of unknown length
            *    63092    74014: contig of 10923 bp in length
            *                   gap of unknown length
            *    74015    86348: contig of 12334 bp in length
            *                   gap of unknown length
            *    86349   102743: contig of 16395 bp in length
            *                   gap of unknown length
            *   102744   129336: contig of 26593 bp in length
            *                   gap of unknown length
            *   129337   178274: contig of 48938 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3p"
                     /clone="RP11-429D11"
ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 12;  Length 178274;
  Best Local Similarity   89.2%;  Pred. No. 0.061;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||||||| | ||||||||| ||||||||||||
Db      77832 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 77868


RESULT 7
AC026168
LOCUS       AC026168               180508 bp    DNA     linear   PRI 11-OCT-2000
DEFINITION  Homo sapiens chromosome 11 clone RP11-156E23 map 11q, complete
            sequence.
ACCESSION   AC026168
VERSION     AC026168.3  GI:10765018
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 180508)
  AUTHORS   Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
            Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
            He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G.,
            Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
            Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S.,
            Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J.,
            Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D.,
            Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
            Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
            Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
  TITLE     Chromosome 11q genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 180508)
  AUTHORS   Kang,N., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
            Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
            Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
            Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
            Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
            and Yang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2000) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
REFERENCE   3  (bases 1 to 180508)
  AUTHORS   Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
            Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
            He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G.,
            Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
            Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S.,
            Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J.,
            Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D.,
            Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
            Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
            Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-2000) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
COMMENT     On Oct 11, 2000 this sequence version replaced gi:8101136.
            --------------Genome Center
            Center:Beijing Center
            Center code:Beijing
            Website:http://hgc.igtp.ac.cn
            http://www.genomics.org.cn
            Contact:hgc@igtp.ac.cn
            -------------- Project Information
            Center project name:1% project
            Center clone name: RP11-156E23
            -------------- Summary Statistics
            Sequencing vector: pUC18; 100% of reads
            Chemistry: Dye-terminator: ET 55% of reads
            Chemistry: Dye-terminator Big Dye; 45% of reads
            Assembly program: Phrap; version 0.990329
            Consensus quality: 183755 bases at least Q40
            Consensus quality: 183944 bases at least Q30
            Consensus quality: 184060 bases at least Q20
            Insert size: 180508; sum-of-contigs
            Quality coverage:  14.44x in Q20 bases;sum-of-contigs
            --------------.
FEATURES             Location/Qualifiers
     source          1. .180508
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="11q"
                     /clone="RP11-156E23"
ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 5;  Length 180508;
  Best Local Similarity   89.2%;  Pred. No. 0.062;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||||||| | ||||||||| ||||||||||||
Db     112270 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 112306
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RESULT 8
AP003030/c
LOCUS       AP003030              180736 bp    DNA     linear   HTG 12-DEC-2000
DEFINITION  Homo sapiens chromosome 11 clone RP11-156E23 map 11q, WORKING DRAFT
            SEQUENCE, 25 unordered pieces.
ACCESSION   AP003030
VERSION     AP003030.1  GI:11691888
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 180736)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens 180,736 genomic DNA of 11q
  JOURNAL   Published Only in DataBase (2000)
REFERENCE   2  (bases 1 to 180736)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-2000) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     -------------- Genome Center
                Center: RIKEN Genomic Sciences Center(GSC)
                Center code: RIKEN
                Web site: http://hgp.gsc.riken.go.jp/
                Contact: hattori@gsc.riken.go.jp
            -------------- Project Information
                Center project name: HumDraft11
                Center clone name: RP11-156E23
            -------------- Summary Statistics
                Sequencing vector: PCR products; 100% of reads
                Chemistry: Dye-terminator ET-amersham; 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 176079 bases at least Q40
                Consensus quality: 177426 bases at least Q30
                Consensus quality: 178052 bases at least Q20
                Insert size: 178336; sum-of-contigs
                Quality coverage: 9.42x in Q20 bases; sum-of-contigs
            --------------.
            NOTE: This is a 'working draft' sequence. It currently consists of
            25 contigs. The true order of the pieces is not known and their
            order in this sequence record is arbitrary. Gaps between the
            contigs are represented as runs N, but the exact sizes of the gaps
            are unknown. This record will be updated with the finished sequence
            as soon as it is available and the accession number will be
            preserved
                  1     17039 contig of  17039 bp in length
              17140     33427 contig of  16288 bp in length
              33528     46545 contig of  13018 bp in length
              46646     58197 contig of  11552 bp in length
              58298     74036 contig of  15739 bp in length
              74137     82961 contig of   8825 bp in length
              83062     93987 contig of  10926 bp in length
              94088     99506 contig of   5419 bp in length
              99607    107756 contig of   8150 bp in length
             107857    115182 contig of   7326 bp in length
             115283    121835 contig of   6553 bp in length
             121936    128404 contig of   6469 bp in length
             128505    134531 contig of   6027 bp in length
             134632    140489 contig of   5858 bp in length
             140590    147926 contig of   7337 bp in length
             148027    152333 contig of   4307 bp in length
             152434    157174 contig of   4741 bp in length
             157275    161451 contig of   4177 bp in length
             161552    165998 contig of   4447 bp in length
             166099    169793 contig of   3695 bp in length
             169894    172504 contig of   2611 bp in length
             172605    175090 contig of   2486 bp in length
             175191    177405 contig of   2215 bp in length
             177506    179103 contig of   1598 bp in length
             179204    180736 contig of   1533 bp in length.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 25 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     17039: contig of 17039 bp in length
            *   17040     17139: gap of 100 bp
            *   17140     33427: contig of 16288 bp in length
            *   33428     33527: gap of 100 bp
            *   33528     46545: contig of 13018 bp in length
            *   46546     46645: gap of 100 bp
            *   46646     58197: contig of 11552 bp in length
            *   58198     58297: gap of 100 bp
            *   58298     74036: contig of 15739 bp in length
            *   74037     74136: gap of 100 bp
            *   74137     82961: contig of 8825 bp in length
            *   82962     83061: gap of 100 bp
            *   83062     93987: contig of 10926 bp in length
            *   93988     94087: gap of 100 bp
            *   94088     99506: contig of 5419 bp in length
            *   99507     99606: gap of 100 bp
            *   99607    107756: contig of 8150 bp in length
            *  107757    107856: gap of 100 bp
            *  107857    115182: contig of 7326 bp in length
            *  115183    115282: gap of 100 bp
            *  115283    121835: contig of 6553 bp in length
            *  121836    121935: gap of 100 bp
            *  121936    128404: contig of 6469 bp in length
            *  128405    128504: gap of 100 bp
            *  128505    134531: contig of 6027 bp in length
            *  134532    134631: gap of 100 bp
            *  134632    140489: contig of 5858 bp in length
            *  140490    140589: gap of 100 bp
            *  140590    147926: contig of 7337 bp in length
            *  147927    148026: gap of 100 bp
            *  148027    152333: contig of 4307 bp in length
            *  152334    152433: gap of 100 bp
            *  152434    157174: contig of 4741 bp in length
            *  157175    157274: gap of 100 bp
            *  157275    161451: contig of 4177 bp in length
            *  161452    161551: gap of 100 bp
            *  161552    165998: contig of 4447 bp in length
            *  165999    166098: gap of 100 bp
            *  166099    169793: contig of 3695 bp in length
            *  169794    169893: gap of 100 bp
            *  169894    172504: contig of 2611 bp in length
            *  172505    172604: gap of 100 bp
            *  172605    175090: contig of 2486 bp in length
            *  175091    175190: gap of 100 bp
            *  175191    177405: contig of 2215 bp in length
            *  177406    177505: gap of 100 bp
            *  177506    179103: contig of 1598 bp in length
            *  179104    179203: gap of 100 bp
            *  179204    180736: contig of 1533 bp in length.
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ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 12;  Length 180736;
  Best Local Similarity   89.2%;  Pred. No. 0.062;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
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Db     127964 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 127928


RESULT 9
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LOCUS       AP006215               189310 bp    DNA     linear   PRI 18-FEB-2003
DEFINITION  Homo sapiens genomic DNA, chromosome 11, clone:RP11-729P6, complete
            sequence.
ACCESSION   AP006215
VERSION     AP006215.1  GI:28411651
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA
  JOURNAL   Published Only in Database (2003)
REFERENCE   2  (bases 1 to 189310)
  AUTHORS   Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-FEB-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
FEATURES             Location/Qualifiers
     source          1. .189310
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="11q"
                     /clone="RP11-729P6"
ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 5;  Length 189310;
  Best Local Similarity   89.2%;  Pred. No. 0.063;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||||||  | |||||||||| ||||||||||||
Db      13890 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 13854


RESULT 10
AC015845/c
LOCUS       AC015845               191957 bp    DNA     linear   PRI 29-JUL-2002
DEFINITION  Homo sapiens chromosome 17, clone RP11-343K8, complete sequence.
ACCESSION   AC015845
VERSION     AC015845.8  GI:22002208
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 191957)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-343K8
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 191957)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
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            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 191957)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
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            Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
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            Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
            Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
            Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
            Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUN-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 191957)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
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            Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
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            Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
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            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jul 29, 2002 this sequence version replaced gi:21362231.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L479
                Center clone name: 343_K_8
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                     /map="17"
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     repeat_region   1612. .1882
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  Query Match             82.7%;  Score 30.6;  DB 5;  Length 191957;
  Best Local Similarity   89.2%;  Pred. No. 0.063;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db       2115 CTGTCTGTCTGCCTCTCTTGTTGCCCAGGCTGGAGTG 2079


RESULT 11
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LOCUS       AC022004              196373 bp    DNA     linear   HTG 03-FEB-2000
DEFINITION  Homo sapiens chromosome 3p clone RP11-369J15, WORKING DRAFT
            SEQUENCE, 27 unordered pieces.
ACCESSION   AC022004
VERSION     AC022004.2  GI:6862657
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 196373)
  AUTHORS   Dong,W., Hu,S., Zhang,X., Wang,J., Wang,X., Zhang,Y., Zhang,H.,
            Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
            Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
            Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L.,
            Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
            Feng,X., Yu,J. and Yang,H.
  TITLE     Chromosome 3p genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 196373)
  AUTHORS   Dong,W., Hu,S., Zhang,X., Wang,J., Wang,X., Zhang,Y., Zhang,H.,
            Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
            Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
            Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L.,
            Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
            Feng,X., Yu,J. and Yang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Human Genomic Center, Institute of
            Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
            100101, P.R.China
COMMENT     On Feb 3, 2000 this sequence version replaced gi:6742905.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 27 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2841: contig of 2841 bp in length
            *                   gap of unknown length
            *     2842     5168: contig of 2327 bp in length
            *                   gap of unknown length
            *     5169     8800: contig of 3632 bp in length
            *                   gap of unknown length
            *     8801    10990: contig of 2190 bp in length
            *                   gap of unknown length
            *    10991    13801: contig of 2811 bp in length
            *                   gap of unknown length
            *    13802    16477: contig of 2676 bp in length
            *                   gap of unknown length
            *    16478    18903: contig of 2426 bp in length
            *                   gap of unknown length
            *    18904    21319: contig of 2416 bp in length
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            *    44154    49473: contig of 5320 bp in length
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            *    49474    54867: contig of 5394 bp in length
            *                   gap of unknown length
            *    54868    60579: contig of 5712 bp in length
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            *    60580    66495: contig of 5916 bp in length
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            *    66496    76922: contig of 10427 bp in length
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            *    76923    86942: contig of 10020 bp in length
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            *    86943    97647: contig of 10705 bp in length
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                     /chromosome="3p"
                     /clone="RP11-369J15"
ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 12;  Length 196373;
  Best Local Similarity   89.2%;  Pred. No. 0.064;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
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Db      22363 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 22399


RESULT 12
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LOCUS       AC024733              225231 bp    DNA     linear   HTG 03-JUN-2001
DEFINITION  Homo sapiens chromosome 11 clone RP11-577L15, WORKING DRAFT
            SEQUENCE, 2 unordered pieces.
ACCESSION   AC024733
VERSION     AC024733.7  GI:14280296
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 225231)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 225231)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Jun 3, 2001 this sequence version replaced gi:9958290.

            ------------------- Genome Center --------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            ---------------- Project Information -----------------
            Center project name: H_NH0577L15
            -----------------------------------------------------
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 37%
            Sequencing vector: plasmid; 63%
            Chemistry: Dye-primer ET; 37% of reads
            Chemistry: Dye-terminator Big Dye; 63% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 224941 bases at least Q40
            Consensus quality: 225083 bases at least Q30
            Consensus quality: 225120 bases at least Q20
            Insert size: 214000; agarose-fp
            Insert size: 225131; sum-of-contigs
            Quality coverage: 10.85 in Q20 bases; agarose-fp
            Quality coverage: 10.75 in Q20 bases; sum-of-contigs
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    31247: contig of 31247 bp in length
            *    31248    31347: gap of unknown length
            *    31348   225231: contig of 193884 bp in length.
FEATURES             Location/Qualifiers
     source          1. .225231
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /clone="RP11-577L15"
     misc_feature    1. .31247
                     /note="assembly_name:Contig5
                     clone_end:SP6
                     vector_side:left"
     gap             31248. .31347
                     /estimated_length=unknown
     misc_feature    31348. .225231
                     /note="assembly_name:Contig6
                     clone_end:T7
                     vector_side:right"
ORIGIN

  Query Match             82.7%;  Score 30.6;  DB 12;  Length 225231;
  Best Local Similarity   89.2%;  Pred. No. 0.067;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
                  |||||||||  | |||||||| ||||||||||||
Db      18421 CTGACTGACTTTCCCTCTTGTTGCCCAGGCTGGAGTG 18457


RESULT 13
BV520177/c
LOCUS       BV520177                857 bp    DNA     linear   STS 08-APR-2005
DEFINITION  G591P66349FF1.T0 Clint Pan troglodytes verus STS genomic, sequence
            tagged site.
ACCESSION   BV520177
VERSION     BV520177.1  GI:62397935
KEYWORDS    STS.
SOURCE      Pan troglodytes verus
  ORGANISM  Pan troglodytes verus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 857)
  AUTHORS   Mikkelsen,T.S., Hillier,W.L., Eichler,E.E., Zody,M.C. and
            Jaffe,D.B.
  TITLE     Initial Sequence of the Chimpanzee Genome and Comparison with the
            Human Genome
  JOURNAL   Unpublished (2005)
COMMENT
            Contact: Michael C. Zody
            Broad Institute of MIT and Harvard
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172580933
            Fax: 6172580903
            Email: mczody@broad.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 857
            Protocol:
            23,021,928 chimpanzee whole genome shotgun reads were aligned to
            the Human genome NCBI
            Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors,
            including Clint (Pan
            troglodytes verus), 3 other Pan troglodytes verus chimps
            (Donald,Karlien,Yvonne), 3 Pan
            troglodytes troglodytes chimps (Noemie,Masuku,Clara) and 2 chimps
            of unknown origin
            (Gon,Unknown Chimp). Common names:  Pan troglodytes verus is the
            western chimp and Pan
            troglodytes troglodytes is the central chimp. To be included in
            chimpanzee SNP discovery, a
            read must be at least 500bp in length, at least 50% of its base
            calls must have Phred
            score >= 20, at least 30% of its base calls must satisfy
            SNQS(30,25)(single strand NQS, the
            base in question has Phred score >= 30, the surrounding 10 bases in
            the read have Phred
            score >= 25), and the read must have at least 200 bp SNQS(30,25)
            bases. Reads not uniquely
            placed in the genome and read pairs whose two ends were not
            consistently placed were
            discarded. After above filtering, NQS(30,25) standard was applied
            to all pairs of
            overlapping reads to call NQS bases and SNPs. Alignments (between
            two reads) with less
            than 100 NQS bases or with SNP rate > 0.01 were discarded. To
            exclude alignment between two
            copies of a single read, comparisons between two reads that share
            95% of their genome
            alignments (>=95% bases of read A and >=95% bases of read B were
            placed at the same locus
            of human genome) were discarded.
FEATURES             Location/Qualifiers
     source          1. .857
                     /organism="Pan troglodytes verus"
                     /mol_type="genomic DNA"
                     /sub_species="verus"
                     /db_xref="taxon:37012"
```

```
                     /clone_lib="Clint"
     STS             <1. .>857
ORIGIN

  Query Match             80.0%;  Score 29.6;  DB 7;  Length 857;
  Best Local Similarity   88.9%;  Pred. No. 0.029;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||| ||||||||||||
Db        630 TGACTGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 595


RESULT 14
BS000175/c
LOCUS       BS000175              183155 bp    DNA     linear   PRI 12-JUN-2004
DEFINITION  Pan troglodytes chromosome 22 clone:PTB-091H17, map 22, complete
            sequences.
ACCESSION   BS000175 BA000046
VERSION     BS000175.1  GI:37537442
KEYWORDS    HTG.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   The International Chimpanzee Chromosome 22 Consortium.
  TITLE     DNA sequence and comparative analysis of chimpanzee chromosome 22
  JOURNAL   Nature 429, 382-388 (2004)
REFERENCE   2  (bases 1 to 183155)
  AUTHORS   Wang,S., Cai,Z., Wang,B., Zheng,H., Zhang,Y., Zhang,X., Zhu,G.,
            Lu,G., Fu,G. and Chen,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAY-2003) Shengyue Wang, Chinese National Human
            Genome Center at Shanghai, Genomic Sequencing; No.250 BiBo Road,
            Zhang Jiang HI-TECH Park, Shanghai 201203, CHINA
            (E-mail:wangsy@chgc.sh.cn, URL:http://www.chgc.sh.cn,
            Tel:86-21-50801919, Fax:86-21-50801922)
COMMENT     The Chimpanzee Chromosome 22 Sequencing Consortium consists of:
            *Chinese National Human Genome Center at Shanghai, Shanghai, China;
            *GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
            of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
            Center, Daejeon, Korea;
            *Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
            *National Institute of Genetics, Mishima, Japan;
            *National Yang Ming University Genome Research Center, Taipei,
            Taiwan;
            *RIKEN Genomic Sciences Center, Yokohama, Japan.
            -------------- Genome Center
            Center: Chinese National Human Genome Center at Shanghai Center
            code: CHGCS
            Web site: http://chgc.sh.cn
            Contact: wangsy@chgc.sh.cn
            -------------- Project Information
            Center project name:The Chimpanzee Chromosome 22 Sequencing Project
            Center clone name: PTB-091H17
            -------------- Summary Statistics
            Sequencing vector: pUC18,100% of reads
            Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly
            program: Phrap; version 0.990329
            Consensus quality:   182579 bases at least Q40
            Consensus quality:   182966 bases at least Q30
            Consensus quality:   183111 bases at least Q20
            Quality coverage: 9.4x
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30);
            an attempt was made to resolve all sequencing problems, such as
            compressions and repeats; all regions were covered by at one
            plasmid
            subclone or more than one M13 subclone;
            and the assembly was confirmed by restriction digest.
            --------------
            Source information:
            The PTB1 chimpanzee BAC library was prepared from DNA isolated from
            cultured cells established from the blood of a single male
            chimpanzee.
            Clones may be obtained from Asao Fujiyama and co-workers
            (http://www.gsc.riken.go.jp).
            VECTOR:  pKS145
            Sequence Quality Assessment:
            This entry has been annotated with sequence
            estimates computed by the Phrap assembly program.
            All manually edited bases have been reduced to quality zero.
            Quality levels above 40 are expected to have less than 1 error in
            10,000 bp.
            ----------------------
            Neighboring clones: PTB-137B16(left) and RP43-006O21(right).
FEATURES              Location/Qualifiers
     source           1. .183155
                      /organism="Pan troglodytes"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9598"
                      /chromosome="22"
                      /clone="PTB-091H17"
                      /clone_lib="PTB1 chimpanzee BAC"
ORIGIN

  Query Match             80.0%;  Score 29.6;  DB 5;  Length 183155;
  Best Local Similarity   88.9%;  Pred. No. 0.18;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||| ||||||||||||
Db     151118 TGACTGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 151083


RESULT 15
AC010329
LOCUS       AC010329              187607 bp    DNA     linear   PRI 18-APR-2000
DEFINITION  Homo sapiens chromosome 19 clone CTD-2626G11, complete sequence.
ACCESSION   AC010329
VERSION     AC010329.3  GI:7328724
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 187607)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 187607)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 187607)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAR-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 187607)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Mar 25, 2000 this sequence version replaced gi:6600837.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
```

```
           Quality: Phrap Quality >=40 100% of Sequence;
           Estimated Total Number of Errors is 0.
FEATURES             Location/Qualifiers
     source          1. .187607
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /clone="CTD-2626G11"
ORIGIN

  Query Match             80.0%;  Score 29.6;  DB 5;  Length 187607;
  Best Local Similarity   88.9%;  Pred. No. 0.18;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| || | ||||||||| |||||||||||||
Db      83620 TGACTGAGTGTCACTCTTGTTGCCCAGGCTGGAGTG 83655


Search completed: July  1, 2006, 00:03:37
Job time : 1367.53 secs
```

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:13:35 ; Search time 4995 Seconds
(without alignments)
414.217 Million cell updates/sec

Title: US-10-615-497-14
Perfect score: 37
Sequence: 1 ctgactgactgactctcttgttgaccaggctggagtg 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	29.6	80.0	188	1	AA513565	AA513565 nh28d05.s
c	2	28	75.7	372	13	CW626404	CW626404 Hsap_13A_
	3	28	75.7	401	2	BF881618	BF881618 QV3-ET019
c	4	28	75.7	499	11	AQ135647	AQ135647 HS_3053_B
c	5	28	75.7	585	11	AQ174114	AQ174114 HS_3200_B
c	6	27.4	74.1	286	10	DW425202	DW425202 HHAGE0249
	7	27.4	74.1	412	1	AA525879	AA525879 ni57f03.s
	8	27.4	74.1	481	3	BM771536	BM771536 K-EST0055
	9	27.4	74.1	483	3	BM756299	BM756299 K-EST0034
	10	27.4	74.1	501	1	AL598011	AL598011 DKFZp313F
	11	27.4	74.1	518	7	AW849972	AW849972 IL3-CT021
c	12	27.4	74.1	538	9	DB140646	DB140646 DB140646
	13	27.4	74.1	615	3	BM766474	BM766474 K-EST0048
	14	27.4	74.1	620	3	BM742390	BM742390 K-EST0015
	15	27.4	74.1	878	7	BE898834	BE898834 601682124
	16	27	73.0	152	1	AI561351	AI561351 tq48d11.x
c	17	27	73.0	188	3	BU536080	BU536080 AGENCOURT
c	18	27	73.0	195	7	BE068181	BE068181 CM2-BT036
	19	27	73.0	197	2	BF895353	BF895353 IL0-MT021
	20	27	73.0	202	1	AF202336	AF202336 AF202336
c	21	27	73.0	215	10	DW446838	DW446838 HHAGE0445
c	22	27	73.0	217	1	AA233685	AA233685 zr43d03.r
	23	27	73.0	218	8	CR740939	CR740939 CR740939
c	24	27	73.0	226	1	AL601995	AL601995 DKFZp313I
	25	27	73.0	237	1	AI972417	AI972417 wr39d11.x
c	26	27	73.0	245	7	AW889465	AW889465 RC6-NT002
	27	27	73.0	251	9	DN848275	DN848275 KECB34-22
	28	27	73.0	258	8	CV317053	CV317053 CM2-BT085
c	29	27	73.0	269	7	AW833528	AW833528 QV4-TT000
c	30	27	73.0	278	7	BE068201	BE068201 CM1-BT036
c	31	27	73.0	280	2	BF934731	BF934731 IL2-NT020
	32	27	73.0	289	2	BF902783	BF902783 IL5-MT020
	33	27	73.0	289	14	AG197617	AG197617 Pan trogl
c	34	27	73.0	294	10	DW422365	DW422365 HHAGE0220
	35	27	73.0	296	1	AA493774	AA493774 nh02c08.s
c	36	27	73.0	299	2	BF809730	BF809730 CM1-CI013
c	37	27	73.0	299	10	DW421001	DW421001 HHAGE0207
c	38	27	73.0	304	7	BE068159	BE068159 CM2-BT036
c	39	27	73.0	313	1	AA665028	AA665028 nu69h04.s
c	40	27	73.0	316	1	AA376557	AA376557 EST88991
c	41	27	73.0	323	3	BU958108	BU958108 AGENCOURT
c	42	27	73.0	325	10	T05143	T05143 EST03031 Fe
	43	27	73.0	336	4	CA946753	CA946753 is10c06.x
c	44	27	73.0	346	10	DW467349	DW467349 HHAGE0086
	45	27	73.0	349	2	BF950367	BF950367 CM3-NN118

ALIGNMENTS

RESULT 1
AA513565
LOCUS AA513565 188 bp mRNA linear EST 19-AUG-1997
DEFINITION nh28d05.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:953673 similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION AA513565
VERSION AA513565.1 GI:2251977
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 188)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 589 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 178.
FEATURES Location/Qualifiers
source 1. .188
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:953673"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr3"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st

strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

ORIGIN

Query Match 80.0%; Score 29.6; DB 1; Length 188;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| || | ||||||||| ||||||||||||||
Db         12 TGACTGAGTGTCGCTCTTGTTGCCCAGGCTGGAGTG 47
```

RESULT 2
CW626404/c
LOCUS CW626404 372 bp DNA linear GSS 02-SEP-2005
DEFINITION Hsap_13A_UR_B08 Hsap Homo sapiens genomic clone Hsap_13A_UR_B08, genomic survey sequence.
ACCESSION CW626404
VERSION CW626404.1 GI:74098177
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Wicker,T., Robertson,J.S., Schulze,S.R., Feltus,F.A., Ivarie,R. and Paterson,A.H.
TITLE Ultra-rapidly associating DNA forms diverse secondary structures with many biological functions
JOURNAL Unpublished (2005)
COMMENT Contact: Paterson AH
Plant Genome Mapping Laboratory
University of Georgia, Center for Applied Genetic Technologies
Riverbend Research Laboratory, Room 162, 110 Riverbend Road, Athens, GA 30602 USA
Tel: 7065830169
Fax: 7065830160
Email: paterson@uga.edu
repetitive sequence (>50 copies in genome)
Plate: Hsap-13A row: B column: 08
Class: unknown.
FEATURES Location/Qualifiers
source 1. .372
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Hsap_13A_UR_B08"
/clone_lib="Hsap"
/note="Vector: pBluescript; Site_1: EcoR1; Site_2: Xho1"

ORIGIN

Query Match 75.7%; Score 28; DB 13; Length 372;
Best Local Similarity 86.1%; Pred. No. 9.5;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  | ||||||||| ||||||||||||||
Db        122 TGACTGAGTTTCACTCTTGTTGCCCAGGCTGGAGTG 87
```

RESULT 3
BF881618

LOCUS BF881618 401 bp mRNA linear EST 17-JAN-2001
DEFINITION QV3-ET0197-041200-501-g02 ET0197 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF881618
VERSION BF881618.1 GI:12271744
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 401)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV3&t2=QV3-ET0197-041200-501-g02&t3=2000-12-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 47
High quality sequence stop: 371.
FEATURES Location/Qualifiers
source 1. .401
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0197"
/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 75.7%; Score 28; DB 2; Length 401;
Best Local Similarity 86.1%; Pred. No. 9.6;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||| || |  |||||||||| ||||||||||||||
Db         44 TGACAGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 79
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RESULT 4
AQ135647/c
LOCUS AQ135647 499 bp DNA linear GSS 24-SEP-1998
DEFINITION HS_3053_B2_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3053 Col=24 Row=L, genomic survey sequence.
ACCESSION AQ135647
VERSION AQ135647.1 GI:3527013
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3053  row: L  column: 24
            Class: BAC ends
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=3053 Col=24 Row=L"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

  Query Match             75.7%;  Score 28;  DB 11;  Length 499;
  Best Local Similarity   86.1%;  Pred. No. 9.9;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| || | |||||||||  ||||||||||||
Db        188 TGACTGAGTGTCACTCTTGTTGCACAGGCTGGAGTG 153


RESULT 5
AQ174114/c
LOCUS       AQ174114                585 bp    DNA     linear   GSS 17-OCT-1998
DEFINITION  HS_3200_B1_G11_T7 CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3200 Col=21 Row=N, genomic survey
            sequence.
ACCESSION   AQ174114
VERSION     AQ174114.1  GI:3571481
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3200  row: N  column: 21
            Class: BAC ends
            High quality sequence stop: 585.
FEATURES             Location/Qualifiers
     source          1. .585
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=3200 Col=21 Row=N"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

  Query Match             75.7%;  Score 28;  DB 11;  Length 585;
  Best Local Similarity   86.1%;  Pred. No. 10;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| || | |||||||||  ||||||||||||
Db         92 TGACTGAGTGTCACTCTTGTTGCACAGGCTGGAGTG 57


RESULT 6
DW425202/c
LOCUS       DW425202                286 bp    mRNA    linear   EST 14-JAN-2006
DEFINITION  HHAGE024932 Human liver regeneration after partial hepatectomy Homo
            sapiens cDNA, mRNA sequence.
ACCESSION   DW425202
VERSION     DW425202.1  GI:84926758
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 286)
  AUTHORS   Xu,C.S.
  TITLE     Liver regeneration after PH
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Cun-Shuan Xu
            Henan Bioengineering Key Lab
            Henan Normal University
            No. 148 Jianshe Road, Xinxiang City, P.R.China
            Tel: 00863733328084
            Fax: 00863733326524
            Email: xucs@x263.net.
FEATURES             Location/Qualifiers
     source          1. .286
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="liver"
                     /clone_lib="Human liver regeneration after partial
                     hepatectomy"
ORIGIN

  Query Match             74.1%;  Score 27.4;  DB 10;  Length 286;
  Best Local Similarity   83.8%;  Pred. No. 15;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | |||||||||| ||||||||||||
Db        234 CTGACGGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 198


RESULT 7
AA525879
LOCUS       AA525879                412 bp    mRNA    linear   EST 05-AUG-1997
DEFINITION  ni57f03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980957
            similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION   AA525879
VERSION     AA525879.1  GI:2267948
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 412)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 508 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 201.
FEATURES Location/Qualifiers
source 1. .412
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:980957"
/sex="female"
/tissue_type="ovary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ov2"
/note="Vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
ORIGIN

Query Match 74.1%; Score 27.4; DB 1; Length 412;
Best Local Similarity 83.8%; Pred. No. 16;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | |||||||| ||||||||||||
Db         19 CTGACAGAGTTTCACTCTTGTTGCCCAGGCTGGAGTG 55
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RESULT 8
BM771536
LOCUS BM771536 481 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0055420 S6SNU620s1 Homo sapiens cDNA clone S6SNU620s1-23-H09 5', mRNA sequence.
ACCESSION BM771536
VERSION BM771536.1 GI:19101151
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 481)
AUTHORS Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J., Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and Kim,N.S.
TITLE Transcriptome analysis of human gastric cancer
JOURNAL Mamm. Genome 16 (12), 942-954 (2005)
PUBMED 16341674
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 23 row: H column: 09
High quality sequence stop: 481.
FEATURES Location/Qualifiers
source 1. .481
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S6SNU620s1-23-H09"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F'"
/clone_lib="S6SNU620s1"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the remaining DNA into competent cells E. coli Top10F' with electroporation method."
ORIGIN

Query Match 74.1%; Score 27.4; DB 3; Length 481;
Best Local Similarity 83.8%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||||| |  |  |||||||| ||||||||||||
Db        427 CTGACTGAGTTTCATTCTTGTTGCCCAGGCTGGAGTG 463
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RESULT 9
BM756299
LOCUS BM756299 483 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0034586 S6SNU620 Homo sapiens cDNA clone S6SNU620-28-H07 5', mRNA sequence.
ACCESSION BM756299
VERSION BM756299.1 GI:19085914
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 483)
AUTHORS Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J.,

```
            Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and
            Kim,N.S.
  TITLE     Transcriptome analysis of human gastric cancer
  JOURNAL   Mamm. Genome 16 (12), 942-954 (2005)
   PUBMED   16341674
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 28  row: H  column: 07
            High quality sequence stop: 483.
FEATURES             Location/Qualifiers
     source          1. .483
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S6SNU620-28-H07"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Scattering floating"
                     /cell_line="SNU-620"
                     /lab_host="Top10F'"
                     /clone_lib="S6SNU620"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match             74.1%;  Score 27.4;  DB 3;  Length 483;
  Best Local Similarity   83.8%;  Pred. No. 17;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||||| |  |  |||||||| ||||||||||||
Db        427 CTGACTGAGTTTCATTCTTGTTGCCCAGGCTGGAGTG 463


RESULT 10
AL598011
LOCUS       AL598011                501 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp313F2318_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
            DKFZp313F2318 5', mRNA sequence.
ACCESSION   AL598011
VERSION     AL598011.1  GI:15160702
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp313F2318) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .501
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp313F2318"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="313 (synonym: hlcc2)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

  Query Match             74.1%;  Score 27.4;  DB 1;  Length 501;
  Best Local Similarity   83.8%;  Pred. No. 17;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| |  | |||||||||| ||||||||||||
Db        173 CAGACTGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 209


RESULT 11
AW849972
LOCUS       AW849972                518 bp    mRNA    linear   EST 19-MAY-2000
DEFINITION  IL3-CT0216-160300-096-F06 CT0216 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW849972
VERSION     AW849972.1  GI:7945489
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=IL3-CT0216-160
            300-096-F06&t3=2000-03-16&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 470.
FEATURES             Location/Qualifiers
     source          1. .518
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/dev_stage="Adult"
/clone_lib="CT0216"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 74.1%; Score 27.4; DB 7; Length 518;
Best Local Similarity 83.8%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | ||||||||| ||||||||||||
Db        458 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 494
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RESULT 12
DB140646/c
LOCUS DB140646 538 bp mRNA linear EST 10-DEC-2005
DEFINITION DB140646 THYMU3 Homo sapiens cDNA clone THYMU3013729 5', mRNA sequence.
ACCESSION DB140646
VERSION DB140646.1 GI:83449302
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 538)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
FEATURES Location/Qualifiers
source 1. .538
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="THYMU3013729"
/tissue_type="thymus"
/clone_lib="THYMU3"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 74.1%; Score 27.4; DB 9; Length 538;
Best Local Similarity 83.8%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | ||||||||| ||||||||||||
Db         52 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 16
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RESULT 13
BM766474
LOCUS BM766474 615 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0048387 S6SNU620s1 Homo sapiens cDNA clone S6SNU620s1-7-E07 5', mRNA sequence.
ACCESSION BM766474
VERSION BM766474.1 GI:19096089
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J., Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and Kim,N.S.
TITLE Transcriptome analysis of human gastric cancer
JOURNAL Mamm. Genome 16 (12), 942-954 (2005)
PUBMED 16341674
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 7 row: E column: 07
High quality sequence stop: 615.
FEATURES Location/Qualifiers
source 1. .615
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S6SNU620s1-7-E07"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F'"
/clone_lib="S6SNU620s1"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the

remaining DNA into competent cells E. coli Top10F' with electroporation method."
ORIGIN

Query Match 74.1%; Score 27.4; DB 3; Length 615;
Best Local Similarity 83.8%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
|||||||| | | |||||||| ||||||||||||
Db 427 CTGACTGAGTTTCATTCTTGTTGCCCAGGCTGGAGTG 463

RESULT 14
BM742390
LOCUS BM742390 620 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0015258 S6SNU620 Homo sapiens cDNA clone S6SNU620-5-D03 5', mRNA sequence.
ACCESSION BM742390
VERSION BM742390.1 GI:19063705
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 620)
AUTHORS Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J., Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and Kim,N.S.
TITLE Transcriptome analysis of human gastric cancer
JOURNAL Mamm. Genome 16 (12), 942-954 (2005)
PUBMED 16341674
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: D column: 03
High quality sequence stop: 620.
FEATURES Location/Qualifiers
source 1. .620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S6SNU620-5-D03"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F'"
/clone_lib="S6SNU620"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
ORIGIN

Query Match 74.1%; Score 27.4; DB 3; Length 620;
Best Local Similarity 83.8%; Pred. No. 17;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
|||||||| | | |||||||| ||||||||||||
Db 427 CTGACTGAGTTTCATTCTTGTTGCCCAGGCTGGAGTG 463

RESULT 15
BE898834
LOCUS BE898834 878 bp mRNA linear EST 29-SEP-2000
DEFINITION 601682124F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3952372 5', mRNA sequence.
ACCESSION BE898834
VERSION BE898834.1 GI:10365711
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM821 row: p column: 05
High quality sequence stop: 783.
FEATURES Location/Qualifiers
source 1. .878
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3952372"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Query Match 74.1%; Score 27.4; DB 7; Length 878;
Best Local Similarity 83.8%; Pred. No. 18;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
|||||||| | | |||||||| ||||||||||||
Db 383 CTGACTGAGTTTCATTCTTGTTGCCCAGGCTGGAGTG 419

Search completed: July 1, 2006, 01:17:52
Job time : 4998 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:12:00 ; Search time 315.425 Seconds
(without alignments)
817.859 Million cell updates/sec

Title: US-10-615-497-14
Perfect score: 37
Sequence: 1 ctgactgactgactctcttgttgaccaggctggagtg 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	37	100.0	37	12	ADO03979	Ado03979 Human CYP
	2	28.6	77.3	816	4	AAI97603	Aai97603 Human neu
	3	28.6	77.3	74371	14	AED18320	Aed18320 Fibrotic
	4	28	75.7	31236	9	ADA02900	Ada02900 Human PTP
	5	28	75.7	31236	10	ADB72638	Adb72638 Human PTP
	6	28	75.7	31236	10	ADC85379	Adc85379 Mouse Ptp
	7	28	75.7	31236	12	ADM74495	Adm74495 Human car
	8	27.4	74.1	412	6	ABL83673	Abl83673 Human ova
c	9	27.4	74.1	107820	4	AAD16230	Aad16230 Human ATP
	10	27.4	74.1	125515	10	ADL13941	Adl13941 Osteoarth
c	11	27.4	74.1	172984	8	ACF62733	Acf62733 Cancer ba
c	12	27.4	74.1	172984	8	ADB20848	Adb20848 MRP1 base
c	13	27.4	74.1	172984	10	ADB87937	Adb87937 Human UGT
c	14	27.4	74.1	172984	10	ADB96920	Adb96920 Human MDR
c	15	27.4	74.1	172984	10	ADB92111	Adb92111 Human MDR
	16	27.4	74.1	173115	14	AED89425	Aed89425 Human bre
c	17	27	73.0	101	3	AAC15051	Aac15051 Human sec
	18	27	73.0	132	3	AAC15032	Aac15032 Human sec
c	19	27	73.0	198	4	AAK82987	Aak82987 Human imm
	20	27	73.0	247	3	AAC03633	Aac03633 Human sec
c	21	27	73.0	280	5	ABA17808	Aba17808 Human ner
c	22	27	73.0	280	5	ABA17809	Aba17809 Human ner
	23	27	73.0	316	3	AAC00372	Aac00372 Human sec
c	24	27	73.0	341	4	AAK56329	Aak56329 Human imm
	25	27	73.0	421	14	ADW81896	Adw81896 MAP3K9 ma
c	26	27	73.0	481	3	AAC27522	Aac27522 Human sec
c	27	27	73.0	484	9	ACH13871	Ach13871 Human adu
c	28	27	73.0	486	4	AAI80463	Aai80463 Human pol
	29	27	73.0	486	5	ADI72610	Adi72610 Human ova
	30	27	73.0	486	5	ADL37749	Adl37749 Human ova
c	31	27	73.0	512	4	AAK67815	Aak67815 Human imm
c	32	27	73.0	513	3	AAA43861	Aaa43861 Human sec
	33	27	73.0	529	14	ACL56520	Acl56520 Human col
	34	27	73.0	590	5	ADL44133	Adl44133 Human ova
	35	27	73.0	736	2	AAX30349	Aax30349 DNA encod
	36	27	73.0	736	10	ADB47791	Adb47791 Novel hum
	37	27	73.0	736	12	ADJ55346	Adj55346 Novel hum
	38	27	73.0	736	14	AED67329	Aed67329 Human EST
c	39	27	73.0	1149	4	AAH32523	Aah32523 Human sec
c	40	27	73.0	1227	2	AAV40525	Aav40525 Homo sapi
c	41	27	73.0	1531	8	ACC00047	Acc00047 Human ups
c	42	27	73.0	1531	12	ADQ22036	Adq22036 Human sof
c	43	27	73.0	1531	12	ADQ17285	Adq17285 Human sof
c	44	27	73.0	1643	6	AAL46216	Aal46216 Human liv
	45	27	73.0	1653	4	AAI59440	Aai59440 Human pol

ALIGNMENTS

RESULT 1
ADO03979
ID ADO03979 standard; DNA; 37 BP.
XX
AC ADO03979;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human CYP2D6 gene polymorphism detecting PCR primer, SNP16.
XX
KW Cytochrome P450 2D6; CYP2D6; polymorphism detection;
KW single nucleotide polymorphism; respiratory system; cystic fibrosis;
KW asthma; bronchitis; adult respiratory distress syndrome;
KW digestive system; cancer; inflammatory bowel disease; Crohn's disease;
KW pancreatitis; skeletal system; rheumatoid arthritis; osteoporosis;
KW spinal muscular atrophy; autoimmune disease; multiple sclerosis;
KW psoriasis; insulin dependent diabetes mellitus;
KW systemic lupus erythematosus; autoimmune haemolytic anaemia;
KW neurological disorder; Alzheimer's disease; Parkinson's disease;
KW schizophrenia; leukaemia; aging; human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2004091909-A1.
XX
PD 13-MAY-2004.
XX
PF 07-JUL-2003; 2003US-00615497.
XX
PR 05-JUL-2002; 2002US-0393967P.
PR 16-JUL-2002; 2002US-0396618P.
XX
PA (HUAN/) HUANG D H.
XX
PI Huang DH;
XX
DR WPI; 2004-374942/35.
XX
PT Identifying pre-selected polymorphisms present in cytochrome P450 2D6
PT gene sequences in samples, by generating a labeled nucleic acid and
PT relating labeled nucleic acid to identity of polymorphism.

XX
PS Claim 33; SEQ ID NO 14; 27pp; English.
XX
CC The invention relates to methods for identifying several pre-selected
CC polymorphisms present in cytochrome P450 2D6 (CYP2D6) gene. The method is
CC useful for identifying pre-selected polymorphisms present in cytochrome
CC P450 2D6 gene sequence, e.g., duplication, deletion, inversion,
CC insertion, translocation, polymorphism resulting in aberrant RNA splicing
CC and a single nucleotide polymorphism. It is useful for selecting a
CC therapeutic drug or its prodrug to treat a subject suffering from a
CC disease or disorder that involves the respiratory system (cystic
CC fibrosis, asthma, bronchitis and adult respiratory distress syndrome),
CC digestive system (cancers, inflammatory bowel disease, Crohn's disease
CC and pancreatitis), skeletal system (rheumatoid arthritis, osteoporosis
CC and spinal muscular atrophy), autoimmune disease (multiple sclerosis,
CC psoriasis, insulin dependent diabetes mellitus, systemic lupus
CC erythematosus and autoimmune haemolytic anaemia), neurological disorders
CC (Alzheimer's disease, Parkinson's disease and schizophrenia), various
CC leukaemias and aging. The present sequence is a PCR primer used for
CC detecting human CYP2D6 gene polymorphism. This sequence is used to
CC illustrate the method of the invention.
XX
SQ Sequence 37 BP; 6 A; 9 C; 11 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 37; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
||||||||||||||||||||||||||||||||||||||
Db 1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37

RESULT 2
AAI97603
ID AAI97603 standard; cDNA; 816 BP.
XX
AC AAI97603;
XX
DT 13-NOV-2001 (first entry)
XX
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 3678.
XX
KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
XX
OS Homo sapiens.
XX
PN WO200166719-A1.
XX
PD 13-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-JP001629.
XX
PR 07-MAR-2000; 2000JP-00159195.
XX
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
XX
PI Nakagawara A;
XX
DR WPI; 2001-565584/63.
XX
PT Nucleic acids originating in gene expressed in human neuroblastoma,
PT useful as probe or primer in diagnosing prognosis of human neuroblastoma,
PT malignancy and susceptibility indicator or tumor marker for anti-cancer
PT agents.
XX
PS Claim 1; Page 2669; 2979pp; Japanese.
XX
CC The invention relates to novel genes (AAI93926-AAI97963) expressed in
CC human neuroblastoma. The nucleic acids are applicable as a probe or
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and
CC susceptibility indicators or tumour markers for anti-cancer agents. The
CC gene information for diagnosing prognosis is related to factors similar
CC to that for N-myc and TrkA genes
XX
SQ Sequence 816 BP; 178 A; 155 C; 174 G; 279 T; 0 U; 30 Other;

Query Match 77.3%; Score 28.6; DB 4; Length 816;
Best Local Similarity 88.6%; Pred. No. 0.12;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
||| |||| |||||||||||| ||||||||||||
Db 59 GACAGACTCTCTCTCTTGTTGCCCAGGCTGGAGTG 93

RESULT 3
AED18320
ID AED18320 standard; DNA; 74371 BP.
XX
AC AED18320;
XX
DT 15-DEC-2005 (first entry)
XX
DE Fibrotic disorder associated polynucleotide SEQ ID NO 571.
XX
KW antiinflammatory; gene therapy; fibrogenesis; gene expression;
KW therapeutic; diagnosis; uterine fibroids; gynecological; inflammation;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2005098041-A2.
XX
PD 20-OCT-2005.
XX
PF 28-MAR-2005; 2005WO-US010257.
XX
PR 26-MAR-2004; 2004US-0556546P.
PR 19-OCT-2004; 2004US-0620444P.
PR 15-DEC-2004; 2004US-0636240P.
XX
PA (UYFL) UNIV FLORIDA RES FOUND INC.
XX
PI Chegini N, Luo X, Ding L, Williams RS;
XX
DR WPI; 2005-703565/72.
XX
PT Identifying a modulator of a gene that is differentially-expressed in
PT fibrotic tissue or during fibrogenesis, or a polypeptide encoded by the
PT gene, in a cell population by contacting the cell population with a test
PT agent.
XX
PS Disclosure; SEQ ID NO 571; 202pp; English.
XX
CC The invention describes a method of identifying a modulator of at least
CC one gene that is differentially-expressed in fibrotic tissue or during
CC fibrogenesis, or a polypeptide encoded by the differentially-expressed
CC gene, in a cell population, comprising contacting the cell population
CC with a test agent, and determining if the test agent modulates the
CC expression of the gene or biological activity of the polypeptide encoded
CC by the gene. Also described are: detecting a fibrotic disorder in a
CC subject; modulating gene expression in fibrotic tissue; and an array
CC comprising a substrate having addresses, where each address has a capture
CC probe that can specifically bind at least one polynucleotide that is
CC differentially expressed in fibrotic disorders, or its complement. The
CC method is useful in identifying a modulator of at least one gene that is
CC differentially-expressed in fibrotic tissue or during fibrogenesis, or a
CC polypeptide encoded by the differentially-expressed gene, in a cell
CC population for preparing a composition for diagnosing or treating
CC fibrotic disorders, e.g. uterine fibrosis. This sequence represents a
CC polynucleotide associated with detection and treatment of fibrotic
CC disorders. Note: This sequence does not appear in the printed
CC specification but has been obtained in electronic format directy from
CC WIPO at ftp.wipo.int/pub/published_pct_sequences.

```
XX
SQ   Sequence 74371 BP; 21903 A; 16601 C; 16494 G; 19155 T; 0 U; 218 Other;

  Query Match            77.3%;  Score 28.6;  DB 14;  Length 74371;
  Best Local Similarity   88.6%;  Pred. No. 0.33;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| |  |||||||||| ||||||||||||
Db      19950 GACTGAATTTCTCTCTTGTTGCCCAGGCTGGAGTG 19984


RESULT 4
ADA02900
ID   ADA02900 standard; DNA; 31236 BP.
XX
AC   ADA02900;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human PTP4A2 carcinoma associated gene, SEQ ID NO:1418.
XX
KW   Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW   prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003057146-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US041414.
XX
PR   26-DEC-2001; 2001US-00035832.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-587068/55.
XX
PT   New recombinant nucleic acid encoding carcinoma associated protein,
PT   useful for preparing compositions for treating carcinomas.
XX
PS   Claim 1; SEQ ID NO 1418; 245pp; English.
XX
CC   The invention relates to recombinant carcinoma associated (CA) nucleic
CC   acid sequences from mouse and human (ADA01482-ADA03094), and to
CC   recombinant carcinoma associated proteins (CAP) encoded by them. The
CC   invention also encompasses expression vectors and host cells comprising a
CC   CA nucleic acid, a polypeptide (especially an antibody) that specifically
CC   binds to the protein, and a biochip comprising CA nucleic acid or
CC   fragments thereof. The sequences of the invention were identified using
CC   oncogenic retroviruses, which insert into the genome of the host organism
CC   at random. Many of these do not carry transduced host oncogenes or
CC   pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC   direct consequence of the effects of proviral integration into host
CC   protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC   carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC   leukaemia) or a propensity to carcinoma by determination of the sequence
CC   of a CA gene, or by determination of CA gene expression in particular
CC   tissues. CA nucleic acids, proteins and antibodies are also useful as
CC   therapeutic agents and in screening and evaluating drug candidates. The
CC   present sequence represents a specifically claimed human CA nucleic acid
CC   sequence of the invention. Note: The complete sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 31236 BP; 8595 A; 6081 C; 6658 G; 9902 T; 0 U; 0 Other;

  Query Match            75.7%;  Score 28;  DB 9;  Length 31236;
  Best Local Similarity   86.1%;  Pred. No. 0.49;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||| || |  |||||||||| ||||||||||||
Db       7008 TGACAGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 7043


RESULT 5
ADB72638
ID   ADB72638 standard; DNA; 31236 BP.
XX
AC   ADB72638;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human PTP4A2 gene.
XX
KW   human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW   cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX
OS   Homo sapiens.
XX
PN   WO2003008583-A2.
XX
PD   30-JAN-2003.
XX
PF   26-DEC-2001; 2001WO-US051291.
XX
PR   02-MAR-2001; 2001US-00798586.
PR   23-OCT-2001; 2001US-00004113.
PR   08-NOV-2001; 2001US-00052482.
PR   30-NOV-2001; 2001US-00997722.
PR   20-DEC-2001; 2001US-00034650.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW,  Engelhard EK;
XX
DR   WPI; 2003-239337/23.
XX
PT   New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
PT   cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
PS   Claim 1; SEQ ID NO 466; 2304pp; English.
XX
CC   The invention relates to a novel recombinant nucleic acid comprising a
CC   nucleotide sequence selected from any of the 660 sequences fully defined
CC   in the specification. A polynucleotide of the invention has cytostatic
CC   activity, and may have a use in gene therapy, or in a vaccine. The
CC   recombinant nucleic acids and polypeptides are useful for treating
CC   carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC   sarcomas. The present sequence represents a human gene of the invention.
XX
SQ   Sequence 31236 BP; 8595 A; 6081 C; 6658 G; 9902 T; 0 U; 0 Other;

  Query Match            75.7%;  Score 28;  DB 10;  Length 31236;
  Best Local Similarity   86.1%;  Pred. No. 0.49;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||| || |  |||||||||| ||||||||||||
Db       7008 TGACAGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 7043


RESULT 6
ADC85379
ID   ADC85379 standard; DNA; 31236 BP.
XX
AC   ADC85379;
XX
DT   01-JAN-2004  (first entry)
XX
```

```
DE   Mouse Ptp4a2 coding sequence.
XX
KW   Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;
KW   secreted; transmembrane; intracellular; ds.
XX
OS   Mus sp.
XX
PN   WO2003045230-A2.
XX
PD   05-JUN-2003.
XX
PF   02-DEC-2002; 2002WO-US038582.
XX
PR   30-NOV-2001; 2001US-00997722.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW,  Engelhard EK;
XX
DR   WPI; 2003-513603/48.
XX
PT   New recombinant nucleic acid comprising a nucleotide sequence of any of
PT   the carcinoma-associated (CA) genes, useful for screening for drug
PT   candidates for diagnosing or treating carcinomas.
XX
PS   Claim 1; SEQ ID NO 165; 983pp; English.
XX
CC   The invention relates to a recombinant nucleic acid comprising a
CC   nucleotide sequence selected from any of the fully defined carcinoma-
CC   associated (CA) genes from the 50 tables given in the specification. The
CC   CA proteins are secreted, transmembrane or intracellular proteins. The
CC   recombinant nucleic acids are useful for screening for drug candidates
CC   for diagnosing or treating carcinomas. Sequences given in ADC85215-
CC   ADC85514 represent CA genes of the invention.
XX
SQ   Sequence 31236 BP; 8595 A; 6081 C; 6658 G; 9902 T; 0 U; 0 Other;

  Query Match             75.7%;  Score 28;  DB 10;  Length 31236;
  Best Local Similarity   86.1%;  Pred. No. 0.49;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||| || |  |||||||||| ||||||||||||
Db       7008 TGACAGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 7043


RESULT 7
ADM74495
ID   ADM74495 standard; DNA; 31236 BP.
XX
AC   ADM74495;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human carcinoma associated (CA) nucleic acid #82.
XX
KW   Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
KW   carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2004072154-A1.
XX
PD   15-APR-2004.
XX
PF   30-NOV-2001; 2001US-00997722.
XX
PR   22-DEC-2000; 2000US-00747377.
PR   02-MAR-2001; 2001US-00798586.
XX
PA   (MORR/) MORRIS D W.
PA   (ENGE/) ENGELHARD E K.
XX
PI   Morris DW,  Engelhard EK;
XX
DR   WPI; 2004-328562/30.
XX
PT   New carcinoma associated gene or protein, useful for preparing a
PT   composition for diagnosing or treating carcinoma e.g., leukemia or
PT   lymphoma.
XX
PS   Claim 1; SEQ ID NO 166; 29pp; English.
XX
CC   The invention relates to new recombinant nucleic acids. The invention
CC   also relates to a host cell comprising a recombinant nucleic acid or
CC   expression vector, an expression vector comprising a recombinant nucleic
CC   acid, a recombinant protein, a method of screening for drug candidates, a
CC   method of screening for a bioactive agent capable of binding to a
CC   carcinoma associated protein (CAP) encoded by a nucleotide sequence, a
CC   method of screening for a bioactive agent capable of modulating the
CC   activity of a CAP, a method of evaluating the effect of a candidate
CC   carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting
CC   the activity of a CAP, a method of treating carcinomas, a method of
CC   neutralising the effect of a CAP and a method of diagnosing carcinoma or
CC   propensity to carcinoma. A method of evaluating the effect of a candidate
CC   carcinoma drug comprises administering the drug to a patient, removing a
CC   cell sample from the patient and determining alterations in the
CC   expression or activation of a gene comprising the nucleotide sequence. A
CC   method of diagnosing carcinoma comprises determining the expression of
CC   one or more genes comprising the nucleic acid sequence in a first tissue
CC   type of a first individual and comparing the expression of the gene from
CC   a second normal tissue type from the first individual or a second
CC   unaffected individual, where a difference in the expression indicates
CC   that the first individual has carcinoma. A method of inhibiting the
CC   activity of a CAP comprises binding an inhibitor to the CAP. Treating
CC   carcinomas comprises administering to a patient an inhibitor of CAP.
CC   Neutralising the effect of a CAP comprises contacting an agent specific
CC   for the CAP. The polypeptide specifically binds to the protein encoded by
CC   the nucleic acid. It comprises an antibody that specifically binds to the
CC   protein encoded by the nucleic acid. The nucleic acids are useful for
CC   preparing a composition for diagnosing or treating carcinoma e.g.,
CC   leukaemia or lymphoma. This sequence represents a human carcinoma
CC   associated (CA) nucleic acid of the invention. Note: The sequence data
CC   for this patent did not form part of the printed specification but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 31236 BP; 8595 A; 6081 C; 6658 G; 9902 T; 0 U; 0 Other;

  Query Match             75.7%;  Score 28;  DB 12;  Length 31236;
  Best Local Similarity   86.1%;  Pred. No. 0.49;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||| || |  |||||||||| ||||||||||||
Db       7008 TGACAGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 7043


RESULT 8
ABL83673
ID   ABL83673 standard; cDNA; 412 BP.
XX
AC   ABL83673;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human ovarian cancer related cDNA clone SEQ ID NO:6651.
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192581-A2.
XX
PD   06-DEC-2001.
```

```
XX
PF   29-MAY-2001; 2001WO-US017756.
XX
PR   26-MAY-2000; 2000US-0207484P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Algate PA,  Harlocker SL,  Jones R;
XX
DR   WPI; 2002-122075/16.
XX
PT   Composition for therapy and diagnosis of ovarian cancer comprising
PT   polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT   polypeptide, antibody specific to polypeptide or T cell expressing
PT   polypeptide.
XX
PS   Claim 1; SEQ ID NO 6651; 489pp; English.
XX
CC   The present invention describes a composition (I) comprising: carriers
CC   and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC   polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
CC   from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
CC   (III) encoding (II) having a sequence (S2), a T cell population of (II),
CC   or antigen presenting cells that express (II). (I) has cytostatic
CC   activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
CC   detecting ovarian cancer in a patient's biological sample preferably
CC   serum or ovarian tissue. The method comprises contacting a biological
CC   sample from a patient with (IV), detecting the amount of polynucleotide
CC   hybridising to (IV) and comparing the amount to a predetermined cutoff
CC   value and thereby detecting ovarian cancer in the patient, where the
CC   amount of polynucleotide hybridising to (IV) is detected preferably by
CC   polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
CC   useful for stimulating and/or expanding T cells specific for an ovarian
CC   tumour protein comprising contacting T cells with (III) or (II). (III) is
CC   useful in design and preparation of ribozyme molecules for inhibiting
CC   expression of the tumour polypeptides and proteins in tumour cells; and
CC   to isolate a full length gene from a suitable library e.g., a tumour cDNA
CC   library using well known techniques
XX
SQ   Sequence 412 BP; 89 A; 100 C; 99 G; 124 T; 0 U; 0 Other;

  Query Match             74.1%;  Score 27.4;  DB 6;  Length 412;
  Best Local Similarity   83.8%;  Pred. No. 0.33;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | |||||||||| ||||||||||||
Db         19 CTGACAGAGTTTCACTCTTGTTGCCCAGGCTGGAGTG 55


RESULT 9
AAD16230/c
ID   AAD16230 standard; DNA; 107820 BP.
XX
AC   AAD16230;
XX
DT   19-NOV-2001  (first entry)
XX
DE   Human ATP-binding cassette transporter ABCC6 (MRP6) complementary gene.
XX
KW   Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW   Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW   ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW   Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   intron          complement(29772. .1)
FT                   /*tag= bl
FT                   /number= 32
FT   exon            complement(29881. .29773)
FT                   /*tag= bk
FT                   /number= 31
FT   intron          complement(30217. .29882)
FT                   /*tag= bj
FT                   /number= 31
FT   exon            complement(30412. .30218)
FT                   /*tag= bi
FT                   /number= 30
FT   intron          complement(34270. .30413)
FT                   /*tag= bh
FT                   /number= 30
FT   exon            complement(34437. .34271)
FT                   /*tag= bg
FT                   /number= 29
FT   intron          complement(34515. .34438)
FT                   /*tag= bf
FT                   /number= 29
FT   exon            complement(34674. .34516)
FT                   /*tag= be
FT                   /number= 28
FT   intron          complement(37306. .34675)
FT                   /*tag= bd
FT                   /number= 28
FT   exon            complement(37453. .37307)
FT                   /*tag= bc
FT                   /number= 27
FT   intron          complement(39124. .37454)
FT                   /*tag= bb
FT                   /number= 27
FT   exon            complement(39226. .39125)
FT                   /*tag= ba
FT                   /number= 26
FT   intron          complement(41082. .39227)
FT                   /*tag= az
FT                   /number= 26
FT   exon            complement(41209. .41083)
FT                   /*tag= ay
FT                   /number= 25
FT   intron          complement(42637. .41210)
FT                   /*tag= ax
FT                   /number= 25
FT   exon            complement(42837. .42638)
FT                   /*tag= aw
FT                   /number= 24
FT   intron          complement(45267. .42838)
FT                   /*tag= av
FT                   /number= 24
FT   exon            complement(45578. .45268)
FT                   /*tag= au
FT                   /number= 23
FT   intron          complement(49380. .45579)
FT                   /*tag= at
FT                   /number= 23
FT   exon            complement(49588. .49381)
FT                   /*tag= as
FT                   /number= 22
FT   intron          complement(52636. .49589)
FT                   /*tag= ar
FT                   /number= 22
FT   exon            complement(52757. .52637)
FT                   /*tag= aq
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FT                   /*tag= ap
FT                   /number= 21
FT   exon            complement(55345. .55270)
FT                   /*tag= ao
FT                   /number= 20
FT   intron          complement(56810. .55346)
FT                   /*tag= an
FT                   /number= 20
FT   exon            complement(56985. .56811)
FT                   /*tag= am
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FT                   /number= 19
FT   intron          complement(58156. .56986)
FT                   /*tag= al
FT                   /number= 19
FT   exon            complement(58324. .58157)
FT                   /*tag= ak
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FT                   /*tag= ai
FT                   /number= 17
FT   intron          complement(62155. .61941)
FT                   /*tag= ah
FT                   /number= 17
FT   exon            complement(62282. .62156)
FT                   /*tag= ag
FT                   /number= 16
FT   intron          complement(64309. .62283)
FT                   /*tag= af
FT                   /number= 16
FT   exon            complement(64385. .64310)
FT                   /*tag= ae
FT                   /number= 15
FT   intron          complement(66474. .64386)
FT                   /*tag= ad
FT                   /number= 15
FT   exon            complement(66562. .66475)
FT                   /*tag= ac
FT                   /number= 14
FT   intron          complement(68181. .66563)
FT                   /*tag= ab
FT                   /number= 14
FT   exon            complement(68325. .68182)
FT                   /*tag= aa
FT                   /number= 13
FT   intron          complement(69514. .68326)
FT                   /*tag= z
FT                   /number= 13
FT   exon            complement(69718. .69515)
FT                   /*tag= y
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FT   intron          complement(72175. .69719)
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FT                   /number= 12
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FT                   /*tag= w
FT                   /number= 11
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FT                   /*tag= v
FT                   /number= 11
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FT                   /*tag= t
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FT   intron          complement(82756. .81525)
FT                   /*tag= r
FT                   /number= 9
FT   exon            complement(82954. .82757)
FT                   /*tag= q
FT                   /number= 8
FT   intron          complement(88075. .82955)
FT                   /*tag= p
FT                   /number= 8
FT   exon            complement(88207. .88076)
FT                   /*tag= o
FT                   /number= 7
FT   intron          complement(91532. .88208)
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FT                   /number= 7
FT   exon            complement(91594. .91533)
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FT   intron          complement(93675. .91595)
FT                   /*tag= l
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FT   intron          complement(98902. .93799)
FT                   /*tag= j
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FT   exon            complement(99031. .98903)
FT                   /*tag= i
FT                   /number= 4
FT   intron          complement(99170. .99032)
FT                   /*tag= h
FT                   /number= 4
FT   exon            complement(99296. .99171)
FT                   /*tag= g
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FT   intron          complement(100997. .99297)
FT                   /*tag= f
FT                   /number= 3
FT   exon            complement(101180. .100998)
FT                   /*tag= e
FT                   /number= 2
FT   intron          complement(102747. .101181)
FT                   /*tag= d
FT                   /number= 2

  Query Match             74.1%;  Score 27.4;  DB 4;  Length 107820;
  Best Local Similarity   83.8%;  Pred. No. 1.1;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | |||||||||| ||||||||||||
Db      79775 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 79739


RESULT 10
ADL13941
ID   ADL13941 standard; DNA; 125515 BP.
XX
AC   ADL13941;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Osteoarthritis-associated polymorphic nucleotide #473.
XX
KW   ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW   joint space narrowing; osteophyte development; joint pain;
KW   osteoarthritis; SNP; single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO2003054166-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-US041225.
XX
PR   20-DEC-2001; 2001US-0342603P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Jones KA,  Schafer A;
XX
DR   WPI; 2003-559141/52.
XX
```

PT Determining susceptibility of an individual to joint space narrowing,
PT osteophyte development and/or joint pain comprises identifying whether
PT the individual has at least one polymorphism in a polynucleotide encoding
PT a protein.
XX
PS Disclosure; SEQ ID NO 473; 297pp; English.
XX
CC The invention relates to a method of determining susceptibility of an
CC individual to joint space narrowing and/or osteophyte development and/or
CC joint pain comprising identifying whether the individual has at least one
CC polymorphism in a polynucleotide encoding at least one of the protein
CC listed in the specification. The methods, composition and agent are
CC useful for modulating the susceptibility of an individual to joint space
CC narrowing and/or osteophyte development and/or joint pain that is
CC associated with a disease, preferably osteoarthritis. The cell line and
CC the non-human animal are useful for screening for an agent for diagnosing
CC an individual having susceptibility to joint space narrowing and/or
CC osteophyte development and/or joint pain. This sequence corresponds to
CC the polynucleotide encoding a protein listed in the specification. (Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 125515 BP; 33180 A; 28822 C; 28744 G; 34769 T; 0 U; 0 Other;

Query Match 74.1%; Score 27.4; DB 10; Length 125515;
Best Local Similarity 83.8%; Pred. No. 1.2;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
||||| || | | ||||||||| ||||||||||||
Db 41490 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 41526

RESULT 11
ACF62733/c
ID ACF62733 standard; DNA; 172984 BP.
XX
AC ACF62733;
XX
DT 08-OCT-2003 (first entry)
XX
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:661.
XX
KW Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; gene; ds.
XX
OS Unidentified.
XX
PN WO2003013534-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008219.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-268144/26.
XX
PT New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
PS Disclosure; SEQ ID NO 661; 86pp; English.
XX
CC The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 172984 BP; 43026 A; 39813 C; 42766 G; 47334 T; 0 U; 45 Other;

Query Match 74.1%; Score 27.4; DB 8; Length 172984;
Best Local Similarity 83.8%; Pred. No. 1.3;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
||||| || | | ||||||||| ||||||||||||
Db 79775 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 79739

RESULT 12
ADB20848/c
ID ADB20848 standard; DNA; 172984 BP.
XX
AC ADB20848;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:661.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW ds.
XX
OS Unidentified.
XX
PN WO2003013533-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008200.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-354397/33.
XX
PT Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a
PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.
XX
PS Disclosure; SEQ ID NO 661; 100pp; English.
XX
CC The present invention describes a method for the use of irinotecan (I) or
CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a multidrug resistance protein 1 (MRP1)
CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human

```
CC   (preferably African or Asian) or a mouse. The present sequence represents
CC   a sequence which is used in the exemplification of the present invention.
XX
SQ   Sequence 172984 BP; 43026 A; 39813 C; 42766 G; 47334 T; 0 U; 45 Other;

  Query Match             74.1%;  Score 27.4;  DB 8;  Length 172984;
  Best Local Similarity   83.8%;  Pred. No. 1.3;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | ||||||||| ||||||||||||
Db      79775 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 79739


RESULT 13
ADB87937/c
ID   ADB87937 standard; DNA; 172984 BP.
XX
AC   ADB87937;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human UGT1A1 gene sequence SEQ ID NO:661.
XX
KW   irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KW   colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KW   ovarian cancer; pancreatic cancer; malignant glioma;
KW   uridine diphosphate glycosyltransferasel member A1; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003013536-A2.
XX
PD   20-FEB-2003.
XX
PF   23-JUL-2002; 2002WO-EP008217.
XX
PR   23-JUL-2001; 2001EP-00117608.
PR   24-MAY-2002; 2002EP-00011710.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Heinrich G,  Kerb R;
XX
DR   WPI; 2003-289896/28.
XX
PT   Use of irinotecan to treat cancer patient by determining if patient has
PT   variant alleles of UGT1A1 gene, administering increased/decreased amounts
PT   of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX
PS   Disclosure; SEQ ID NO 661; 107pp; English.
XX
CC   The invention relates to the novel use of irinotecan to treat a patient
CC   suffering from cancer. This involves determining if the patient has one
CC   or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC   more of such variant alleles, irinotecan is administered in an increased
CC   or decreased amount in comparison to the amount that is administered
CC   without regard to the patient's alleles in the UGT1A1 gene. The invention
CC   has cytostatic activity. A composition of the invention acts as a
CC   topoisomerase I inhibitor. The method is useful for treating a patient,
CC   an animal e.g. mouse or a human, preferably African or Asian, suffering
CC   from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC   pancreatic cancer or malignant glioma. The present sequence is udes in
CC   the exemplification of the invention.
XX
SQ   Sequence 172984 BP; 43026 A; 39813 C; 42766 G; 47334 T; 0 U; 45 Other;

  Query Match             74.1%;  Score 27.4;  DB 10;  Length 172984;
  Best Local Similarity   83.8%;  Pred. No. 1.3;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | ||||||||| ||||||||||||
Db      79775 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 79739


RESULT 14
ADB96920/c
ID   ADB96920 standard; DNA; 172984 BP.
XX
AC   ADB96920;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human MDR1 related DNA sequence SEQ ID NO:661.
XX
KW   irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW   lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW   multidrug resistance 1; MDR1; cytostatic; human; Cyp3A5; MRP1; MDR1;
KW   TOP1; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003013537-A2.
XX
PD   20-FEB-2003.
XX
PF   23-JUL-2002; 2002WO-EP008218.
XX
PR   23-JUL-2001; 2001EP-00117608.
PR   24-MAY-2002; 2002EP-00011710.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Heinrich G,  Kerb R;
XX
DR   WPI; 2003-268145/26.
XX
PT   New use of irinotecan for preparation of pharmaceutical compositions for
PT   treating cancer in subject having genome with variant allele comprising
PT   multidrug resistance 1 polynucleotide.
XX
PS   Disclosure; SEQ ID NO 661; 130pp; English.
XX
CC   The invention relates to the novel use of irinotecan or its derivative
CC   for the preparation of pharmaceutical compositions for treating
CC   colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC   malignant glioma in a subject having a genome with a variant allele which
CC   comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC   of the invention has cytostatic activity. The invention is useful for the
CC   preparation of pharmaceutical compositions for treating colorectal,
CC   cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC   glioma in a subject (preferably human, more preferably African or Asian)
CC   or a mouse. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 172984 BP; 43026 A; 39813 C; 42766 G; 47334 T; 0 U; 45 Other;

  Query Match             74.1%;  Score 27.4;  DB 10;  Length 172984;
  Best Local Similarity   83.8%;  Pred. No. 1.3;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | ||||||||| ||||||||||||
Db      79775 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 79739


RESULT 15
ADB92111/c
ID   ADB92111 standard; DNA; 172984 BP.
XX
AC   ADB92111;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human MDR1 related DNA sequence SEQ ID NO:661.
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XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytostatic; human; UGT1A1; MRP1; TOP1; ds.
XX
OS Homo sapiens.
XX
PN WO2003013535-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008220.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-342400/32.
XX
PT New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; SEQ ID NO 661; 104pp; English.
XX
CC The invention relates ro a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 172984 BP; 43026 A; 39813 C; 42766 G; 47334 T; 0 U; 45 Other;

Query Match 74.1%; Score 27.4; DB 10; Length 172984;
Best Local Similarity 83.8%; Pred. No. 1.3;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | ||||||||| ||||||||||||
Db      79775 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 79739
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Search completed: July 1, 2006, 00:41:25
Job time : 319.425 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 23:02:15 ; Search time 890.312 Seconds
(without alignments)
510.655 Million cell updates/sec

Title: US-10-615-497-14
Perfect score: 37
Sequence: 1 ctgactgactgactctcttgttgaccaggctggagtg 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	37	100.0	37	8	US-10-615-497-14	Sequence 14, Appl
c	2	30.6	82.7	1233	6	US-10-027-632-123661	Sequence 123661,
c	3	30.6	82.7	1233	7	US-10-027-632-123661	Sequence 123661,
c	4	28.6	77.3	650	12	US-10-301-480-573541	Sequence 573541,
c	5	28.6	77.3	650	12	US-10-301-480-1186950	Sequence 1186950,
	6	28.6	77.3	684	12	US-10-301-480-535070	Sequence 535070,
	7	28.6	77.3	684	12	US-10-301-480-1148479	Sequence 1148479,
c	8	28.2	76.2	526	4	US-09-925-065A-224005	Sequence 224005,
c	9	28.2	76.2	526	5	US-09-925-065A-224005	Sequence 224005,
c	10	28.2	76.2	551	12	US-10-301-480-308876	Sequence 308876,
c	11	28.2	76.2	551	12	US-10-301-480-922285	Sequence 922285,
c	12	28.2	76.2	2597	12	US-10-301-480-40714	Sequence 40714, A
c	13	28.2	76.2	2597	12	US-10-301-480-654123	Sequence 654123,
	14	28	75.7	535	4	US-09-925-065A-822257	Sequence 822257,
	15	28	75.7	535	5	US-09-925-065A-822257	Sequence 822257,
c	16	28	75.7	647	4	US-09-925-065A-794261	Sequence 794261,
c	17	28	75.7	647	5	US-09-925-065A-794261	Sequence 794261,
c	18	28	75.7	986	12	US-10-301-480-597862	Sequence 597862,
c	19	28	75.7	986	12	US-10-301-480-1211271	Sequence 1211271,
c	20	28	75.7	987	12	US-10-301-480-597863	Sequence 597863,
c	21	28	75.7	987	12	US-10-301-480-1211272	Sequence 1211272,
c	22	28	75.7	1094	4	US-09-925-065A-725915	Sequence 725915,
c	23	28	75.7	1094	5	US-09-925-065A-725915	Sequence 725915,
	24	28	75.7	31236	3	US-09-997-722-166	Sequence 166, App
c	25	27.6	74.6	206739	10	US-10-981-277-49	Sequence 49, Appl
c	26	27.4	74.1	120	8	US-10-242-535A-29961	Sequence 29961, A
c	27	27.4	74.1	120	8	US-10-085-783A-29961	Sequence 29961, A
	28	27.4	74.1	412	3	US-09-867-701-6651	Sequence 6651, Ap
	29	27.4	74.1	665	12	US-10-301-480-567470	Sequence 567470,
	30	27.4	74.1	665	12	US-10-301-480-1180879	Sequence 1180879,
	31	27.4	74.1	666	12	US-10-301-480-566720	Sequence 566720,
	32	27.4	74.1	666	12	US-10-301-480-1180129	Sequence 1180129,
c	33	27.4	74.1	805	4	US-09-925-065A-34435	Sequence 34435, A
c	34	27.4	74.1	805	5	US-09-925-065A-34435	Sequence 34435, A
c	35	27.4	74.1	805	12	US-10-301-480-135673	Sequence 135673,
c	36	27.4	74.1	805	12	US-10-301-480-749082	Sequence 749082,
	37	27.4	74.1	1777	6	US-10-027-632-98375	Sequence 98375, A
	38	27.4	74.1	1777	7	US-10-027-632-98375	Sequence 98375, A
	39	27.4	74.1	57181	9	US-10-741-600-17781	Sequence 17781, A
	40	27.4	74.1	57181	10	US-10-995-561-13350	Sequence 13350, A
c	41	27.4	74.1	107820	3	US-09-792-616-1	Sequence 1, Appli
c	42	27.4	74.1	107820	8	US-10-764-328-1	Sequence 1, Appli
c	43	27.4	74.1	172984	9	US-10-484-577-661	Sequence 661, App
	44	27.4	74.1	173115	15	US-11-112-908-65	Sequence 65, Appl
	45	27	73.0	200	4	US-09-925-065A-471693	Sequence 471693,

ALIGNMENTS

RESULT 1
US-10-615-497-14
; Sequence 14, Application US/10615497
; Publication No. US20040091909A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: HIGH THROUGHPUT CYTOCHROME P450 GENOTYPING
; FILE REFERENCE: 034827-1303
; CURRENT APPLICATION NUMBER: US/10/615,497
; CURRENT FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-615-497-14

Query Match 100.0%; Score 37; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
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RESULT 2
US-10-027-632-123661/c
; Sequence 123661, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

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;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123661
;   LENGTH: 1233
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-123661

  Query Match             82.7%;  Score 30.6;  DB 6;  Length 1233;
  Best Local Similarity   89.2%;  Pred. No. 0.017;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| ||| ||| |||||||||||| ||||||||||||
Db        610 CTGTCTGTCTGCCTCTCTTGTTGCCCAGGCTGGAGTG 574


RESULT 3
US-10-027-632-123661/c
; Sequence 123661, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123661
;   LENGTH: 1233
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-123661

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  Best Local Similarity   89.2%;  Pred. No. 0.017;
  Matches   33;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| ||| ||| |||||||||||| ||||||||||||
Db        610 CTGTCTGTCTGCCTCTCTTGTTGCCCAGGCTGGAGTG 574


RESULT 4
US-10-301-480-573541/c
; Sequence 573541, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 573541
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-573541

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  Best Local Similarity   88.6%;  Pred. No. 0.11;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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              ||||||||  | |||||||||| ||||||||||||
Db        648 GACTGACTTTCGCTCTTGTTGCCCAGGCTGGAGTG 614


RESULT 5
US-10-301-480-1186950/c
; Sequence 1186950, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1186950
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-1186950

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  Best Local Similarity   88.6%;  Pred. No. 0.11;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||||  | |||||||||| ||||||||||||
Db        648 GACTGACTTTCGCTCTTGTTGCCCAGGCTGGAGTG 614


RESULT 6
US-10-301-480-535070
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; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
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;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
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;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 535070
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-535070

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  Best Local Similarity   88.6%;  Pred. No. 0.11;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | || |||||||||| ||||||||||||
Db        198 GACTGAGTTACCCTCTTGTTGCCCAGGCTGGAGTG 232


RESULT 7
US-10-301-480-1148479
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; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1148479
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-1148479

  Query Match             77.3%;  Score 28.6;  DB 12;  Length 684;
  Best Local Similarity   88.6%;  Pred. No. 0.11;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | || |||||||||| ||||||||||||
Db        198 GACTGAGTTACCCTCTTGTTGCCCAGGCTGGAGTG 232


RESULT 8
US-09-925-065A-224005/c
; Sequence 224005, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 224005
;   LENGTH: 526
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-224005

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  Best Local Similarity   85.7%;  Pred. No. 0.16;
  Matches   30;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | :| |||||||||| ||||||||||||
Db        275 GACTGAGTTWCGCTCTTGTTGCCCAGGCTGGAGTG 241


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; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 224005
;   LENGTH: 526
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-224005

  Query Match             76.2%;  Score 28.2;  DB 5;  Length 526;
  Best Local Similarity   85.7%;  Pred. No. 0.16;
  Matches   30;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | :| |||||||||| ||||||||||||
Db        275 GACTGAGTTWCGCTCTTGTTGCCCAGGCTGGAGTG 241


RESULT 10
US-10-301-480-308876/c
; Sequence 308876, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
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;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 308876
;    LENGTH: 551
;    TYPE: DNA
;    ORGANISM: Homo sapien
US-10-301-480-308876

  Query Match             76.2%;  Score 28.2;  DB 12;  Length 551;
  Best Local Similarity   85.7%;  Pred. No. 0.16;
  Matches   30;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | :| ||||||||| ||||||||||||
Db        300 GACTGAGTTWCGCTCTTGTTGCCCAGGCTGGAGTG 266


RESULT 11
US-10-301-480-922285/c
; Sequence 922285, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 922285
;    LENGTH: 551
;    TYPE: DNA
;    ORGANISM: Homo sapien
US-10-301-480-922285

  Query Match             76.2%;  Score 28.2;  DB 12;  Length 551;
  Best Local Similarity   85.7%;  Pred. No. 0.16;
  Matches   30;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | :| ||||||||| ||||||||||||
Db        300 GACTGAGTTWCGCTCTTGTTGCCCAGGCTGGAGTG 266


RESULT 12
US-10-301-480-40714/c
; Sequence 40714, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40714
;    LENGTH: 2597
;    TYPE: DNA
;    ORGANISM: Homo sapien
US-10-301-480-40714

  Query Match             76.2%;  Score 28.2;  DB 12;  Length 2597;
  Best Local Similarity   85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | :| ||||||||| ||||||||||||
Db       1248 GACTGAGTTWCGCTCTTGTTGCCCAGGCTGGAGTG 1214


RESULT 13
US-10-301-480-654123/c
; Sequence 654123, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 654123
;    LENGTH: 2597
;    TYPE: DNA
;    ORGANISM: Homo sapien
US-10-301-480-654123

  Query Match             76.2%;  Score 28.2;  DB 12;  Length 2597;
  Best Local Similarity   85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | :| ||||||||| ||||||||||||
Db       1248 GACTGAGTTWCGCTCTTGTTGCCCAGGCTGGAGTG 1214


RESULT 14
US-09-925-065A-822257
; Sequence 822257, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 822257
;    LENGTH: 535
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-925-065A-822257

  Query Match             75.7%;  Score 28;  DB 4;  Length 535;
  Best Local Similarity   86.1%;  Pred. No. 0.19;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
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Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| ||| |  |||||||||||| ||||||||||||
Db        485 TGAGTGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 520


RESULT 15
US-09-925-065A-822257
; Sequence 822257, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 822257
;   LENGTH: 535
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-822257

  Query Match             75.7%;  Score 28;  DB 5;  Length 535;
  Best Local Similarity   86.1%;  Pred. No. 0.19;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| ||| |  |||||||||||| ||||||||||||
Db        485 TGAGTGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 520


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GenCore version 5.1.9

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Perfect score: 37
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	28.6	77.3	200033	7	US-11-266-748A-23936	Sequence 23936, A
2	27.4	74.1	1000	7	US-11-266-748A-282828	Sequence 282828,
c 3	27.4	74.1	1000	7	US-11-266-748A-309468	Sequence 309468,
4	27.4	74.1	1000	7	US-11-266-748A-392388	Sequence 392388,
c 5	27.4	74.1	1000	7	US-11-266-748A-483106	Sequence 483106,
c 6	27	73.0	557	7	US-11-266-748A-81021	Sequence 81021, A
7	27	73.0	557	7	US-11-266-748A-133832	Sequence 133832,
c 8	27	73.0	728	7	US-11-266-748A-49080	Sequence 49080, A
c 9	27	73.0	1000	7	US-11-266-748A-200335	Sequence 200335,
10	27	73.0	1000	7	US-11-266-748A-201228	Sequence 201228,
c 11	27	73.0	1000	7	US-11-266-748A-223731	Sequence 223731,
c 12	27	73.0	1000	7	US-11-266-748A-282773	Sequence 282773,
c 13	27	73.0	1000	7	US-11-266-748A-291763	Sequence 291763,
14	27	73.0	1000	7	US-11-266-748A-309413	Sequence 309413,
15	27	73.0	1000	7	US-11-266-748A-343192	Sequence 343192,
c 16	27	73.0	1000	7	US-11-266-748A-392298	Sequence 392298,
c 17	27	73.0	1000	7	US-11-266-748A-403286	Sequence 403286,
18	27	73.0	1000	7	US-11-266-748A-474332	Sequence 474332,
19	27	73.0	1000	7	US-11-266-748A-483016	Sequence 483016,
20	27	73.0	3207	7	US-11-266-748A-26030	Sequence 26030, A
c 21	27	73.0	6175	6	US-10-517-441-97	Sequence 97, Appl
22	27	73.0	35331	7	US-11-266-748A-22882	Sequence 22882, A
c 23	27	73.0	113456	7	US-11-266-748A-58942	Sequence 58942, A
c 24	27	73.0	184666	7	US-11-266-748A-23088	Sequence 23088, A
c 25	27	73.0	201144	7	US-11-266-748A-23494	Sequence 23494, A
c 26	27	73.0	340000	7	US-11-266-748A-61353	Sequence 61353, A
27	26.4	71.4	1000	7	US-11-266-748A-117752	Sequence 117752,
c 28	26.4	71.4	1000	7	US-11-266-748A-159916	Sequence 159916,
c 29	26.4	71.4	1000	7	US-11-266-748A-195429	Sequence 195429,
30	26.4	71.4	1000	7	US-11-266-748A-197535	Sequence 197535,
31	26.4	71.4	1000	7	US-11-266-748A-290059	Sequence 290059,
c 32	26.4	71.4	1000	7	US-11-266-748A-341488	Sequence 341488,
33	26.4	71.4	209216	7	US-11-266-748A-23277	Sequence 23277, A
c 34	26.4	71.4	209216	7	US-11-266-748A-23277	Sequence 23277, A
c 35	26.4	71.4	1237661	7	US-11-266-748A-29041	Sequence 29041, A
36	26	70.3	1000	7	US-11-266-748A-196443	Sequence 196443,
c 37	25.8	69.7	1000	7	US-11-266-748A-202233	Sequence 202233,
38	25.8	69.7	1000	7	US-11-266-748A-295793	Sequence 295793,
c 39	25.8	69.7	1000	7	US-11-266-748A-347222	Sequence 347222,
40	25.8	69.7	1000	7	US-11-266-748A-408804	Sequence 408804,
c 41	25.8	69.7	1000	7	US-11-266-748A-479850	Sequence 479850,
c 42	25.8	69.7	12963	6	US-10-517-441-68	Sequence 68, Appl
43	25.8	69.7	84539	7	US-11-266-748A-31827	Sequence 31827, A
44	25.8	69.7	347503	7	US-11-266-748A-23474	Sequence 23474, A
45	25.4	68.6	436	7	US-11-266-748A-219442	Sequence 219442,

ALIGNMENTS

RESULT 1
US-11-266-748A-23936/c
; Sequence 23936, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23936
; LENGTH: 200033
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23936

Query Match 77.3%; Score 28.6; DB 7; Length 200033;
Best Local Similarity 88.6%; Pred. No. 0.13;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| | |||||||||||| ||||||||||||
Db     116808 GACTGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 116774
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RESULT 2
US-11-266-748A-282828

; Sequence 282828, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 282828
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-282828

Query Match 74.1%; Score 27.4; DB 7; Length 1000;
Best Local Similarity 83.8%; Pred. No. 0.13;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||  || |  |||||||||| ||||||||||||
Db         33 CTGATGGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 69
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RESULT 3
US-11-266-748A-309468/c
; Sequence 309468, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 309468
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-309468

Query Match 74.1%; Score 27.4; DB 7; Length 1000;
Best Local Similarity 83.8%; Pred. No. 0.13;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||  || |  |||||||||| ||||||||||||
Db        968 CTGATGGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 932
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RESULT 4
US-11-266-748A-392388
; Sequence 392388, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 392388
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-392388

Query Match 74.1%; Score 27.4; DB 7; Length 1000;
Best Local Similarity 83.8%; Pred. No. 0.13;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||  || |  |||||||||| ||||||||||||
Db         33 CTGATGGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 69
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RESULT 5
US-11-266-748A-483106/c
; Sequence 483106, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same

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;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 483106
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-483106

  Query Match             74.1%;  Score 27.4;  DB 7;  Length 1000;
  Best Local Similarity   83.8%;  Pred. No. 0.13;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||  || |  |||||||||||| ||||||||||||
Db        968 CTGATGGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 932


RESULT 6
US-11-266-748A-81021/c
; Sequence 81021, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81021
;   LENGTH: 557
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (72)..(95)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-81021

  Query Match             73.0%;  Score 27;  DB 7;  Length 557;
  Best Local Similarity   85.7%;  Pred. No. 0.17;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||  |  | ||||||||| ||||||||||||
Db         68 GACTGAATTTCACTCTTGTTGCCCAGGCTGGAGTG 34


RESULT 7
US-11-266-748A-133832
; Sequence 133832, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 133832
;   LENGTH: 557
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (463)..(486)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-133832

  Query Match             73.0%;  Score 27;  DB 7;  Length 557;
  Best Local Similarity   85.7%;  Pred. No. 0.17;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||  |  | ||||||||| ||||||||||||
Db        490 GACTGAATTTCACTCTTGTTGCCCAGGCTGGAGTG 524


RESULT 8
US-11-266-748A-49080/c
; Sequence 49080, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
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;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49080
;   LENGTH: 728
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-49080

  Query Match             73.0%;  Score 27;  DB 7;  Length 728;
  Best Local Similarity   85.7%;  Pred. No. 0.18;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| |  | ||||||||| ||||||||||||
Db        224 GACTGAATTTCACTCTTGTTGCCCAGGCTGGAGTG 190


RESULT 9
US-11-266-748A-200335/c
; Sequence 200335, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200335
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-200335

  Query Match             73.0%;  Score 27;  DB 7;  Length 1000;
  Best Local Similarity   85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| || || | ||||||||| ||||||||||||
Db        485 GACAGAGTGTCACTCTTGTTGCCCAGGCTGGAGTG 451


RESULT 10
US-11-266-748A-201228
; Sequence 201228, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 201228
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-201228

  Query Match             73.0%;  Score 27;  DB 7;  Length 1000;
  Best Local Similarity   85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| || |  |||||||||| ||||||||||||
Db        921 GACAGAGTCTCTCTCTTGTTGCCCAGGCTGGAGTG 955


RESULT 11
US-11-266-748A-223731/c
; Sequence 223731, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
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;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 223731
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-223731

  Query Match            73.0%;  Score 27;  DB 7;  Length 1000;
  Best Local Similarity  85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| || |  |||||||||||| ||||||||||||
Db        994 GACAGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 960


RESULT 12
US-11-266-748A-282773/c
; Sequence 282773, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 282773
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-282773

  Query Match            73.0%;  Score 27;  DB 7;  Length 1000;
  Best Local Similarity  85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| |||| | |||||||||| ||||||||||||
Db        666 GACGGACTTTCGCTCTTGTTGCCCAGGCTGGAGTG 632


RESULT 13
US-11-266-748A-291763/c
; Sequence 291763, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 291763
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-291763

  Query Match            73.0%;  Score 27;  DB 7;  Length 1000;
  Best Local Similarity  85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| || |  |||||||||| ||||||||||||
Db        994 GACAGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 960


RESULT 14
US-11-266-748A-309413
; Sequence 309413, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
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;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 309413
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-309413

  Query Match             73.0%;  Score 27;  DB 7;  Length 1000;
  Best Local Similarity   85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| ||||  | |||||||||| ||||||||||||
Db        335 GACGGACTTTCGCTCTTGTTGCCCAGGCTGGAGTG 369


RESULT 15
US-11-266-748A-343192
; Sequence 343192, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 343192
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-343192

  Query Match             73.0%;  Score 27;  DB 7;  Length 1000;
  Best Local Similarity   85.7%;  Pred. No. 0.19;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| || |  |||||||||| ||||||||||||
Db          7 GACAGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 41


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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 22:17:54 ; Search time 144.762 Seconds
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Title: US-10-615-497-14
Perfect score: 37
Sequence: 1 ctgactgactgactctcttgttgaccaggctggagtg 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	28.6	77.3	187580	3	US-09-949-016-13266	Sequence 13266, A
	3	28	75.7	601	3	US-09-949-016-179687	Sequence 179687,
	4	28	75.7	601	3	US-09-949-016-179688	Sequence 179688,
	5	28	75.7	601	3	US-09-949-016-179689	Sequence 179689,
	6	28	75.7	601	3	US-09-949-016-179690	Sequence 179690,
	7	28	75.7	601	3	US-09-949-016-179691	Sequence 179691,
	8	28	75.7	601	3	US-09-949-016-179692	Sequence 179692,
	9	28	75.7	69701	3	US-09-949-016-14187	Sequence 14187, A
	10	28	75.7	73308	3	US-09-949-016-16326	Sequence 16326, A
	11	28	75.7	390416	3	US-09-949-016-16923	Sequence 16923, A
	12	27.4	74.1	465	3	US-09-621-976-3394	Sequence 3394, Ap
c	13	27.4	74.1	107820	3	US-09-792-616-1	Sequence 1, Appli
	14	27.4	74.1	260286	3	US-09-949-016-17037	Sequence 17037, A
	15	27.4	74.1	260293	3	US-09-949-016-12106	Sequence 12106, A
c	16	27	73.0	101	3	US-09-513-999C-19126	Sequence 19126, A
	17	27	73.0	132	3	US-09-513-999C-19107	Sequence 19107, A
	18	27	73.0	247	3	US-09-513-999C-3631	Sequence 3631, Ap
	19	27	73.0	316	3	US-09-513-999C-370	Sequence 370, App
	20	27	73.0	440	3	US-09-621-976-11368	Sequence 11368, A
c	21	27	73.0	481	3	US-09-513-999C-31597	Sequence 31597, A
	22	27	73.0	601	3	US-09-949-016-34405	Sequence 34405, A
c	23	27	73.0	601	3	US-09-949-016-36749	Sequence 36749, A
c	24	27	73.0	601	3	US-09-949-016-38957	Sequence 38957, A
c	25	27	73.0	601	3	US-09-949-016-38958	Sequence 38958, A
	26	27	73.0	601	3	US-09-949-016-61047	Sequence 61047, A
	27	27	73.0	601	3	US-09-949-016-61048	Sequence 61048, A
	28	27	73.0	601	3	US-09-949-016-61845	Sequence 61845, A
	29	27	73.0	601	3	US-09-949-016-64609	Sequence 64609, A
c	30	27	73.0	601	3	US-09-949-016-73504	Sequence 73504, A
c	31	27	73.0	601	3	US-09-949-016-79764	Sequence 79764, A
c	32	27	73.0	601	3	US-09-949-016-109428	Sequence 109428,
c	33	27	73.0	601	3	US-09-949-016-109429	Sequence 109429,
	34	27	73.0	601	3	US-09-949-016-118207	Sequence 118207,
c	35	27	73.0	601	3	US-09-949-016-130313	Sequence 130313,
c	36	27	73.0	601	3	US-09-949-016-150070	Sequence 150070,
c	37	27	73.0	601	3	US-09-949-016-154808	Sequence 154808,
	38	27	73.0	601	3	US-09-949-016-156782	Sequence 156782,
	39	27	73.0	601	3	US-09-949-016-183354	Sequence 183354,
	40	27	73.0	601	3	US-09-949-016-199951	Sequence 199951,
	41	27	73.0	601	3	US-09-949-002-2663	Sequence 2663, Ap
	42	27	73.0	601	3	US-09-949-002-2664	Sequence 2664, Ap
	43	27	73.0	601	3	US-09-949-002-2665	Sequence 2665, Ap
	44	27	73.0	601	3	US-09-949-002-5300	Sequence 5300, Ap
	45	27	73.0	601	3	US-09-949-002-5301	Sequence 5301, Ap

ALIGNMENTS

RESULT 1
US-09-949-016-12211/c
; Sequence 12211, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12211
; LENGTH: 85368
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12211

Query Match 77.3%; Score 28.6; DB 3; Length 85368;
Best Local Similarity 88.6%; Pred. No. 0.072;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||| |  | ||||||||||||||||||||||
Db      73454 GACTGAGTTTCACTCTTGTTGACCAGGCTGGAGTG 73420
```

RESULT 2
US-09-949-016-13266
; Sequence 13266, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13266
;   LENGTH: 187580
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(187580)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13266

  Query Match             77.3%;  Score 28.6;  DB 3;  Length 187580;
  Best Local Similarity   88.6%;  Pred. No. 0.087;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||||| ||||||||||||
Db     130321 GACTGAGTTTCTCTCTTGTTGCCCAGGCTGGAGTG 130355


RESULT 3
US-09-949-016-179687
; Sequence 179687, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179687
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-179687

  Query Match             75.7%;  Score 28;  DB 3;  Length 601;
  Best Local Similarity   86.1%;  Pred. No. 0.038;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||||| ||| |||||||||
Db        374 TGACTGAGTTTCTCTCTTGTTGCCCAAGCTGGAGTG 409


RESULT 4
US-09-949-016-179688
; Sequence 179688, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179688
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-179688

  Query Match             75.7%;  Score 28;  DB 3;  Length 601;
  Best Local Similarity   86.1%;  Pred. No. 0.038;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||||| ||| |||||||||
Db        370 TGACTGAGTTTCTCTCTTGTTGCCCAAGCTGGAGTG 405


RESULT 5
US-09-949-016-179689
; Sequence 179689, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179689
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-179689

  Query Match             75.7%;  Score 28;  DB 3;  Length 601;
  Best Local Similarity   86.1%;  Pred. No. 0.038;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||||| ||| |||||||||
Db        368 TGACTGAGTTTCTCTCTTGTTGCCCAAGCTGGAGTG 403


RESULT 6
US-09-949-016-179690
; Sequence 179690, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179690
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-179690

  Query Match             75.7%;  Score 28;  DB 3;  Length 601;
  Best Local Similarity   86.1%;  Pred. No. 0.038;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||||| ||| |||||||||
Db        366 TGACTGAGTTTCTCTCTTGTTGCCCAAGCTGGAGTG 401


RESULT 7
US-09-949-016-179691
; Sequence 179691, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179691
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-179691

  Query Match             75.7%;  Score 28;  DB 3;  Length 601;
  Best Local Similarity   86.1%;  Pred. No. 0.038;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||||| ||| |||||||||
Db        364 TGACTGAGTTTCTCTCTTGTTGCCCAAGCTGGAGTG 399


RESULT 8
US-09-949-016-179692
; Sequence 179692, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179692
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-179692

  Query Match             75.7%;  Score 28;  DB 3;  Length 601;
  Best Local Similarity   86.1%;  Pred. No. 0.038;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||||| ||| |||||||||
Db        226 TGACTGAGTTTCTCTCTTGTTGCCCAAGCTGGAGTG 261


RESULT 9
US-09-949-016-14187
; Sequence 14187, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14187
;   LENGTH: 69701
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14187

  Query Match             75.7%;  Score 28;  DB 3;  Length 69701;
  Best Local Similarity   86.1%;  Pred. No. 0.12;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||| ||||  | ||||||||| ||||||||||||
Db      13786 TGACCGACTTTCACTCTTGTTGCCCAGGCTGGAGTG 13821


RESULT 10
US-09-949-016-16326
; Sequence 16326, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16326
;   LENGTH: 73308
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16326

  Query Match             75.7%;  Score 28;  DB 3;  Length 73308;
  Best Local Similarity   86.1%;  Pred. No. 0.12;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||| ||||  | |||||||||| ||||||||||||
Db      13626 TGACCGACTTTCACTCTTGTTGCCCAGGCTGGAGTG 13661
```

RESULT 11
US-09-949-016-16923
; Sequence 16923, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16923
; LENGTH: 390416
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16923

Query Match 75.7%; Score 28; DB 3; Length 390416;
Best Local Similarity 86.1%; Pred. No. 0.18;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          2 TGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||||| |  |||||||||| ||| |||||||||
Db      95577 TGACTGAGTTTCTCTCTTGTTGCCCAAGCTGGAGTG 95612
```

RESULT 12
US-09-621-976-3394
; Sequence 3394, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3394
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 176..355
; NAME/KEY: misc_feature
; LOCATION: 21
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-3394

Query Match 74.1%; Score 27.4; DB 3; Length 465;
Best Local Similarity 83.8%; Pred. No. 0.064;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              |||||||| |  |  |||||||| ||||||||||||
Db        424 CTGACTGAGTTTCATTCTTGTTGCCCAGGCTGGAGTG 460
```

RESULT 13
US-09-792-616-1/c
; Sequence 1, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 107820
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" can be an A or a T or a G or a C
US-09-792-616-1

Query Match 74.1%; Score 27.4; DB 3; Length 107820;
Best Local Similarity 83.8%; Pred. No. 0.24;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||||| || |  | |||||||||| ||||||||||||
Db      79775 CTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTG 79739
```

RESULT 14
US-09-949-016-17037
; Sequence 17037, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17037
; LENGTH: 260286
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17037

Query Match 74.1%; Score 27.4; DB 3; Length 260286;
Best Local Similarity 83.8%; Pred. No. 0.3;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| | ||||  | |||||||||| ||||||||||||
Db      38314 CTGTCGGACTTTCGCTCTTGTTGCCCAGGCTGGAGTG 38350
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RESULT 15
US-09-949-016-12106
; Sequence 12106, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12106
; LENGTH: 260293
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12106

Query Match 74.1%; Score 27.4; DB 3; Length 260293;
Best Local Similarity 83.8%; Pred. No. 0.3;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 CTGACTGACTGACTCTCTTGTTGACCAGGCTGGAGTG 37
              ||| | ||||  | |||||||||| ||||||||||||
Db      38322 CTGTCGGACTTTCGCTCTTGTTGCCCAGGCTGGAGTG 38358
```

Search completed: July 1, 2006, 01:23:14
Job time : 146.762 secs